

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:00:40 ; Search time 29.3505 Seconds
(without alignments)
2351.779 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804

Sequence: 1 MGIWTLPLVLTSLVARLSS.....KDTSDSENSFRNEIQSLV 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	86.0	331	6 Q9TSN4	Q9tsn4 macaca fasc
2	1531	84.9	331	6 Q9BDN0	Q9bdn0 macaca neme
3	1521	84.3	331	6 Q9BDN4	Q9bdn4 cercocobus
4	1509	83.6	333	6 Q9BDP2	Q9bdp2 macaca mula
5	1500	83.1	331	6 Q9GK36	Q9gk36 macaca assa
6	1492.5	82.7	334	6 Q9GL40	Q9gl40 macaca mula
7	1439.5	79.8	310	6 Q9GK28	Q9gk28 macaca arct
8	1377.5	76.4	328	6 Q9BDP0	Q9bdp0 aotus trivi
9	1052.5	58.3	320	6 Q9XS29	Q9xs29 oryctolagus
10	1052	58.3	319	6 Q9RV79	Q9rv79 oryctolagus
11	967	53.6	327	6 Q97491	Q97491 ovis aries
12	614.5	34.1	263	6 Q9XS60	Q9xs60 oryctolagus
13	481.5	26.7	150	11 Q9R230	Q9r230 rattus norv
14	478	26.5	147	6 Q8SQ52	Q8sq52 felis silve
15	470	26.1	285	13 Q9DGH7	Q9dgh7 gallus gall
16	463.5	25.7	312	13 Q9DGH8	Q9dgh8 gallus gall

17	429.5	23.8	124	6 Q8SQ51	Q8sq51 felis silve
18	286	15.9	65	6 Q8SQ49	Q8sq49 felis silve
19	246	13.6	357	13 Q9DF34	Q9df34 brachydanio
20	226.5	12.6	368	13 Q57408	Q57408 meleagris g
21	212.5	11.8	438	13 Q9DFV0	Q9dfv0 brachydanio
22	208.5	11.6	387	13 Q9PVD4	Q9pvd4 xenopus lae
23	199	11.0	368	13 Q9IAR7	Q9iar7 gallus gall
24	198	11.0	283	6 Q9XS28	Q9xs28 cercopithec
25	189	10.5	368	13 Q9PW79	Q9pw79 gallus gall
26	180	10.0	276	13 Q9DD2	Q9dd2 gallus gall
27	179	9.9	401	13 Q9PRG7	Q9prg7 xenopus lae
28	171	9.5	413	11 Q99MM1	Q99mm1 mus musculu
29	170.5	9.5	446	6 Q9SND3	Q9snd3 felis silve
30	168	9.3	186	12 Q9YP87	Q9yp87 cowpox viru
31	163	9.0	186	12 Q9WJB4	Q9wjb4 vaccinia vi
32	161.5	9.0	169	11 Q9JKE0	Q9jke0 rattus norv
33	161.5	9.0	326	12 Q57120	Q57120 cowpox viru
34	161	8.9	186	12 Q72735	Q72735 cowpox viru
35	161	8.9	186	12 Q911R5	Q911r5 vaccinia vi
36	159.5	8.8	350	12 Q57123	Q57123 cowpox viru
37	158.5	8.8	278	6 Q8SQ34	Q8sq34 sus scrofa
38	155.5	8.6	387	11 Q8VD70	Q8vd70 mus musculu
39	153.5	8.5	326	12 Q57122	Q57122 cowpox viru
40	153	8.5	349	12 Q57098	Q57098 camelpox vi
41	153	8.5	349	12 Q8UYA7	Q8uya7 camelpox vi
42	153	8.5	349	12 Q57284	Q57284 camelpox vi
43	152	8.4	347	12 Q57119	Q57119 cowpox viru
44	151.5	8.4	349	12 Q57100	Q57100 monkeypox v
45	151.5	8.4	349	12 Q57102	Q57102 monkeypox v

ALIGNMENTS

RESULT 1

Q9TSN4	ID	Q9TSN4	PRELIMINARY;	PRT;	331 AA.
AC	Q9TSN4;				
DT	01-MAY-2000 (TReMBLrel. 13, Created)				
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)				
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)				
DE	Death receptor Fas (APO-1/CD95).				
GN	FAS.				
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;				
OC	Cercopitheciae; Macaca.				
OX	NCBI_TaxID=9541;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20237686; PubMed=10773350;				
RA	Murayama Y., Terao K., Inoue-Murayama M.;				
RT	"Molecular cloning and characterization of cynomolgus monkey Fas.";				
RL	Hum. Immunol. 61:474-485(2000).				
DR	EMBL; AB031420; BAA83551.1; -				
DR	HSSP; P25445; 1DDF.				
DR	InterPro; IPR000488; Death.				
DR	InterPro; IPR001368; TNFR_c6.				
DR	Pfam; PF00531; death; 1.				
DR	Pfam; PF00020; TNFR_c6; 2.				
DR	SMART; SM00005; DEATH; 1.				
DR	SMART; SM00208; TNFR; 2.				
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.				
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.				
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.				
KW	Receptor.				
SQ	SEQUENCE 331 AA; 37265 MW; OC61750808IB05DF CRC64;				

Query Match 86.0%; Score 1552; DB 6; Length 331;

Best Local Similarity 87.2%; Pred. No. 2.2e-121;

Matches 292; Conservative 14; Mismatches 25; Indels 4; Gaps 2;

QY 1 MGIWTLPLVLTSLVARLSSVNAQVTDINSKGLRLKTKVTVTETONLEGLHHDGFCH 60

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Db 1 MGIWTLPLVLTSTVRLSKVCNAQVTDISSKGFELRKIVTTTQNLGLHGGQFCR 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRCLCDHGGLVEINCT 120
Db 61 NPCPPGERKARDCTVNEDEPCVPCQEGKEYTDKGHFSSKRCRRCLCDHGGLVEINCT 120
Qy 121 RTQNTKCRCKPNFCNSVCHCDPCTKCEHGIIECTLTNTKCKEEDSRDLPLWCLL 180
Db 121 RTQNTKCRCKPNFCNSVCHCDPCTKCEHGIIECTLTNTKCKEEDSRDLPLWCLL 180
Qy 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPTVAINLSDVLSKYIITAGVM 240
Db 181 LLLPIPIVYV---VKKACRKRKENOGSHESPTLNPTVAINLSDVLSKYIITAGM 236
Qy 241 TLSQVKDFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDTLIKDLK 300
Db 237 TLSQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDTLIKGLT 296
Qy 301 ANLCTLAEKIQTIIKIDTSDSENSFRNEIQTSLV 335
Db 297 ADLCTLAEKIHAVILKIDTSDSENSFRNEIQTSLV 331
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RESULT 2

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Q9BDNO PRELIMINARY; PRT; 331 AA.
AC Q9BDNO;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE FAS antigen CD95.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21383618; PubMed-11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344850; AAK37610.1; -.
DR HSSP; P25445; IDDP.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 44 44 I -> V.
FT VARIANT 47 47 R -> Q.
FT VARIANT 55 55 E -> D.
FT VARIANT 60 60 R -> H.
FT VARIANT 61 61 N -> S.
FT VARIANT 77 77 E -> G.
FT VARIANT 95 95 G -> A.
FT VARIANT 282 282 E -> G.
FT VARIANT 298 298 G -> D.
FT VARIANT 300 300 C -> *.
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;
```

Query Match 84.9%; Score 1531; DB 6; Length 331;
Best Local Similarity 85.7%; Pred. No. 1.2e-119;
Matches 287; Conservative 17; Mismatches 27; Indels 4; Gaps 2;

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Qy 1 MGIWTLPLVLTSTVRLSKVCNAQVTDISSKGFELRKIVTTTQNLGLHGGQFCR 60
Db 1 MGIWTLPLVLTSTVRLSKVCNAQVTDISSKGFELRKIVTTTQNLGLHGGQFCR 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRCLCDHGGLVEINCT 120
Db 61 NPCPPGERKARDCTVNEDEPCVPCQEGKEYTDKGHFSSKRCRRCLCDHGGLVEINCT 120
Qy 121 RTQNTKCRCKPNFCNSVCHCDPCTKCEHGIIECTLTNTKCKEEDSRDLPLWCLL 180
Db 121 RTQNTKCRCKPNFCNSVCHCDPCTKCEHGIIECTLTNTKCKEEDSRDLPLWCLL 180
```

```
Qy 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPTVAINLSDVLSKYIITAGVM 240
Db 181 LLLPIPIVYV---VKKACRKRKENOGSHESPTLNPTVAINLSDVLSKYIITAGM 236
Qy 241 TLSQVKDFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDTLIKDLK 300
Db 237 TLSQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDTLIKGLT 296
Qy 301 ANLCTLAEKIQTIIKIDTSDSENSFRNEIQTSLV 335
Db 297 ADLCTLAEKIHAVILKIDTSDSENSFRNEIQTSLV 331
```

RESULT 3

```
Q9BDN4 PRELIMINARY; PRT; 331 AA.
AC Q9BDN4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE FAS antigen CD95.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21383618; PubMed-11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344843; AAK37602.1; -.
DR HSSP; P25445; IDDP.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 44 44 I -> V.
FT VARIANT 47 47 R -> Q.
FT VARIANT 55 55 E -> D.
FT VARIANT 60 60 R -> H.
FT VARIANT 61 61 N -> S.
FT VARIANT 77 77 E -> G.
FT VARIANT 95 95 G -> A.
FT VARIANT 282 282 E -> G.
FT VARIANT 298 298 G -> D.
FT VARIANT 300 300 C -> *.
SQ SEQUENCE 331 AA; 37277 MW; 1D843C4DE1D343F4 CRC64;
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Query Match 84.3%; Score 1521; DB 6; Length 331;
Best Local Similarity 85.4%; Pred. No. 8.5e-119;
Matches 286; Conservative 17; Mismatches 28; Indels 4; Gaps 2;

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Qy 1 MGIWTLPLVLTSTVRLSKVCNAQVTDISSKGFELRKIVTTTQNLGLHGGQFCR 60
Db 1 MGIWTLPLVLTSTVRLSKVCNAQVTDISSKGFELRKIVTTTQNLGLHGGQFCR 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRCLCDHGGLVEINCT 120
Db 61 NPCPPGERKARDCTVNEDEPCVPCQEGKEYTDKGHFSSKRCRRCLCDHGGLVEINCT 120
Qy 121 RTQNTKCRCKPNFCNSVCHCDPCTKCEHGIIECTLTNTKCKEEDSRDLPLWCLL 180
Db 121 RTQNTKCRCKPNFCNSVCHCDPCTKCEHGIIECTLTNTKCKEEDSRDLPLWCLL 180
```


DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	Fas antigen.
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Shui B., Chi L., Zhang Y.R.;
RT	"Cloning and sequencing of Rhesus monkey Fas antigen cDNA";
RL	Submitted (AUG-2000) to the EMBL/genBank/DBJ databases.
DR	EMBL; AY007572; AAG16762.1; ..
DR	HSSP; P25445; 1DDF.
DR	InterPro; IPR000488; Death..
DR	InterPro; IPR001368; TNFR_C6.
DR	Pfam; PF00531; death; 1.
DR	Pfam; PF00020; TNFR_C6; 2.
DR	SMART; SM00005; DEATH; 1.
DR	SMART; SM00208; TNFR; 2.
DR	PROSITE; PS0017; DEATH DOMAIN; 1.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PS0050; TNFR_NGFR_2; 2.
SQ	SEQUENCE 334 AA; 37531 MW; 2DC5B1661C3191C6 CRC64;

Query Match	82.7%	Score 1492.5;	DB 6;	Length 334;
Best Local Similarity	84.0%;	Pred. No. 2e-116;		
Matches 284;	Conservative 17;	Mismatches 30;	Indels 7;	Gaps

QY	1	MLGIWTLPLVLTSVARLSKSNVAQVTDINSKGLERKTVTVTETQNLEGLHHDGFCH	60
Db	1	MLGTWTLLPLVLTSWRLLSKCVTAQVTDISSRGFLRKIVTITETQNLEGLHHGQPCR	60
QY	61	KPCPPGERKARDCTVNGDEPDCCVQCQEGKEYTKAHFSKKRCRCRLCDDEGHGLEVEIN	120
Db	61	NPCPPGERKARDCTVNEDEPDCCVQCQEGKEYTDKGHFSSKRCRCRLCDDEGHGLEVEIN	120
QY	121	RTQNTKCRCKPNFCNVTCVECHDPCPKCEHGIIKECTLTSTNKCKEGRSRLGWLC--	178
Db	121	RTQNTKCRCKPNFCNSAVCEHCDPTCKAHGIIIECTLTSTNKCKEEDRSRLWLCLL	180
QY	179	-LLLLPIPLIYWKRKEVKQTKRRHKRNKGSHESPTLNPTVAIINSLDVDSLYKITTTA	237
Db	181	LLLLLLLPIIVIV---VIKKPKRRHKRNKGPHESITTLNPET-AINLSDVDLSKYITTTA	236
QY	238	GVMTLSOVKGFVRKNGVNEAKIDEIKNDVNQDTAEQKVOLLNRWNHOLHGKKEAYDTLIK	297
Db	237	GAWTLISOVKDFGRKNVGESEAKIDEIKNDVNQDTAEQKVOLLNRWYQPHGKDCACTLI	296
QY	298	LKANLCITLAERTQTILDKDITSDNSNSFRNEIOSIV	335
Db	297	LKTADLCTLAEKTHAVILDKDITSNTENSFGNEIQNLV	334

RESULT 7	
Q9GK28	
ID	Q9GK28 PRELIMINARY; PRT; 310 AA.
AC	Q9GK28;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Fas antigen APO-1/CD95.
GN	FAS.
OS	Macaca arctoides (Stump-tailed macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
OX	NCBI_TaxID=9540;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;


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DR PROSITE; PS00652; TNFR_NGFR_1; 1.  
DR PROSITE; PS00652; TNFR_NGFR_2; 2.  
FT VARIANT; 157 157  
SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;  
  
Query Match 76.4%; Score 1377.5; DB 6; Length 328;  
Best Local Similarity 78.7%; Pred. No. 7.6e-107;  
Matches 266; Conservative 21; Mismatches 38; Indels 13; Gaps 5;  
  
QY 1 MGIWTLPLVLTSLVARSLSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 60  
DB 1 MGIWTLPLVLTSLVARSLSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 59  
QY 61 KCPGPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 120  
DB 60 KPCSPGKARDCTVNGDEPDCVPCQEGKEYTDKSHSPKRCRRCLDEGHGVEINCT 119  
QY 121 RTQNTKRCRCPNFCNSTVCEHCDPCTCKEHIIECTLSNTKCKEGRSNIW-LCL 179  
DB 120 RTQNTKRCRCPNFCNSTVCEHCDPCTCKEHIIECTLSNTKCKEGRSNIW-LCL 179  
QY 180 LLLPIPLIVVKKREVQKTCRKHKENOGSHESPTLNPTVAINLSVDLSKYITTIAGV 239  
DB 180 LLLPIPLIVVKKREVQKTCRKHKENOGSHESPTLNPTVAINLSVDLSKYITTIAGV 239  
QY 240 MTSQVRGFKVKNVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDPLIKDLK 299  
DB 235 MTSQVRGFKVKNVNEAKIDEIKNDNIKDTAEQVOLLRNWHQHGKKEAYDPLIKDLK 294  
QY 300 KANLCTLAETKIOTIILDKDITSDSENSNFR--NETQSLV 335  
DB 295 KANLTALVERIQNIIRK----DSSENSNRQENQSMV 328  
  
RESULT 9  
Q9XS29 Q9XS29 PRELIMINARY; PRT; 320 AA.  
AC Q9XS29;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE C-type Fas antigen.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Isono T., Tanbe Y., Nagano Y., Seto A.;  
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB021299; BAA78431.1; -  
DR EMBL; AB021296; BAA78428.1; -  
DR HSP; P25445; IDDF.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR001368; TNFR_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR_c6; 3.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00017; DEATH_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.  
DR PROSITE; PS00652; TNFR_NGFR_2; 2.  
DR PROSITE; PS00650; TNFR_NGFR_2; 2.  
SQ SEQUENCE 320 AA; 36102 MW; DA235E243220FFB3 CRC64;  
  
Query Match 58.3%; Score 1052.5; DB 6; Length 320;  
Best Local Similarity 61.1%; Pred. No. 9e-80;  
Matches 204; Conservative 36; Mismatches 69; Indels 25; Gaps 5;  
  
QY 1 MGIWTLPLVLTSLVARSLSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 60  
DB 1 MGIWTLPLVLTSLVARSLSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 45  
  
Query Match 58.3%; Score 1052; DB 6; Length 319;  
Best Local Similarity 61.7%; Pred. No. 9.9e-80;  
Matches 206; Conservative 35; Mismatches 67; Indels 26; Gaps 6;  
  
QY 1 MGIWTLPLVLTSLVARSLSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 60  
DB 1 MGIWTLPLVLTSLVARSLSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 45  
QY 61 KCPGPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 120  
DB 46 QLCPPGTGKKADCTSNBEGKPCQEGKEYTDKSHSPKRCRRCLDEGHGVEINCT 105  
QY 121 RTQNTKRCRCPNFCNSTVCEHCDPCTCKEHIIECTLSNTKCKEGRSNIW-LCL 176  
DB 120 RTQNTKRCRCPNFCNSTVCEHCDPCTCKEHIIECTLSNTKCKEGRSNIW-LCL 176  
QY 106 TIQNTKRCRCPNFCNSTVCEHCDPCTCKEHIIECTLSNTKCKEGRSNIW-LCL 165  
DB 106 TIQNTKRCRCPNFCNSTVCEHCDPCTCKEHIIECTLSNTKCKEGRSNIW-LCL 165  
QY 177 LCLLLPIPLIVVKKREVQKTCRKHKENOGSHESPTLNPTVAINLSVDLSKYITTI 236  
DB 177 LCLLLPIPLIVVKKREVQKTCRKHKENOGSHESPTLNPTVAINLSVDLSKYITTI 236  
QY 166 LSTLL-LPIVLGLRR-----YKHKRDKHGKDYKSTALIPBEGVPMNFSVDISKYIPTI 218  
DB 166 LSTLL-LPIVLGLRR-----YKHKRDKHGKDYKSTALIPBEGVPMNFSVDISKYIPTI 218  
QY 237 AGVMTLSQVGFVKRKNVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDPLIK 296  
DB 237 AGVMTLSQVGFVKRKNVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDPLIK 296
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DT	01-NOV-1999 (TREMBLrel. 12, Created)	
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	Fas antigen spliced variant	
DE	Oryctolagus cuniculus (Rabbit).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
NCBI_TaxID=9986;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Isoro T., Tanbe Y., Nagano Y., Seto A.;	
RT	"Splicing and allelic variation in the rabbit Fas antigen gene.";	
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AB021297; BAA78429.1; -	
DR	HSSP; O14763; 1D4V.	
DR	InterPro: IPR001368; TNFR_c6.	
DR	Pfam: PF00020; TNFR_c6; 3.	
DR	SMART; SM00208; TNFR; 3.	
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.	
DR	PROSITE; PS00050; TNFR_NGFR_2.	
SQ	SEQUENCE 263 AA; 30374 MW; 6D76782ADED1BFD7 CRC64;	
QY	1 MGIWTLPLVLTISVARLSKSNVAQYTDINSKGLERKTVTVETONLEGLHHDGQFCH 60	
Db	1 MGIWVLLPLILTLTASLSTSI-----DCKIRN-----ETQYSTG-VLISGNFCC 45	
QY	61 KPCPPGERKARDCTVNGEDPCVPCQSGKEYTDKAHFFSKRCRCRLCDGEGHGLEIVEINCT 120	
Db	46 QLCPPGTKKKADCTSNBKPDCPCQGBGEYTDKSHFFSKRCRCRLCDGEGHGLEIVETDCT 105	
QY	121 RFQNTKCRCKPNFCNTVGEHCDPTCKCBGHIIECTLTSTNCKEE-----GSRSNLGV 170	
Db	106 TIQNTKCRCKSNFFCNALKCEHCDPTCMCEHGIIECTQTSNTKCKEKGSTTGSKHHFLW 165	
QY	177 LCILLPLPLVWVKREVKQTKRKRKENQGSHPSTLNP 217	
Db	166 LCILLPLPIVLGR-----YKHRDGHGKYDKSTALIP 200	
RESULT 13		
Q9R230		
ID	Q9R230 PRELIMINARY; PRT; 150 AA.	
AC	Q9R230;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	Fas receptor (Fragment).	
DE	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
NCBI_TaxID=10116;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	STRAIN-WISTAR; TISSUE-CORPUS LUTEUM;	
RT	Lareu R.R., Dharmarajan A.;	
RL	"Cloning and expression of Fas and Fas Ligand in the apoptotic rat corpus luteum.";	
DR	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF104034; AAD20221.1; -	
DR	HSSP; P25942; 1CDF.	
DR	InterPro: IPR001368; TNFR_c6.	
DR	Pfam; PF00020; TNFR_c6; 2.	
DR	SMART; SM00208; TNFR; 2.	
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.	
DR	PROSITE; PS00050; TNFR_NGFR_2; 1.	
DR	Receptor.	
NON_TER	1	
NON_TER	150	
SEQUENCE	150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;	

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:57:39 ; Search time 54.3354 seconds
(without alignments)
801.926 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWIAVPLVLVLAGSOLVRH.....KDLGKSTPTDGTENEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	327	14	AA1980.DAT
2	1804	100.0	327	16	AA1982.DAT
3	1804	100.0	327	17	AA1983.DAT
4	1800	99.8	327	20	AA1934.DAT
5	1800	99.8	327	20	AA1934.DAT
6	1001	55.5	576	16	AA1981.DAT
7	981	54.4	592	17	AA1982.DAT
8	977	54.2	169	16	AA1986.DAT
9	863.5	47.9	669	19	AA1999.DAT
10	856	47.5	335	13	AA1980.DAT

11	856	47.5	335	16	AA1980.DAT
12	856	47.5	335	17	AA1982.DAT
13	856	47.5	335	17	AA1983.DAT
14	856	47.5	335	18	AA1984.DAT
15	856	47.5	335	19	AA1985.DAT
16	856	47.5	335	21	AA1934.DAT
17	856	47.5	335	21	AA1934.DAT
18	856	47.5	335	22	AA1935.DAT
19	844	46.8	335	21	AA1936.DAT
20	825	45.7	331	22	AA1989.DAT
21	810.5	44.9	314	16	AA1982.DAT
22	810.5	44.9	314	17	AA1983.DAT
23	801.5	44.4	314	20	AA1980.DAT
24	676.5	37.5	170	21	AA1982.DAT
25	645	35.8	281	21	AA1986.DAT
26	585	32.4	219	22	AA1987.DAT
27	530	29.4	173	21	AA1982.DAT
28	530	29.4	600	16	AA1980.DAT
29	523	29.0	237	21	AA1934.DAT
30	520	28.8	600	17	AA1982.DAT
31	494.5	27.4	144	18	AA1980.DAT
32	494.5	27.4	159	18	AA1982.DAT
33	494.5	27.4	376	18	AA1982.DAT
34	494.5	27.4	376	19	AA1983.DAT
35	482	26.7	86	23	AA1985.DAT
36	341	18.9	431	22	AA1986.DAT
37	340.5	18.9	920	22	AA1986.DAT
38	339	18.8	927	22	AA1986.DAT
39	332	18.4	436	21	AA1982.DAT
40	319.5	17.7	436	22	AA1986.DAT
41	305.5	16.9	149	17	AA1983.DAT
42	281	15.6	121	23	AA1981.DAT
43	278.5	15.4	111	23	AA1981.DAT
44	226	12.5	84	22	AA1986.DAT
45	220	12.2	84	19	AA1982.DAT

ALIGNMENTS

RESULT 1	
AA1980.DAT	
ID	AA1980.DAT standard; Protein: 327 AA.
XX	AA1980.DAT
AC	AA1980.DAT
XX	19-APR-1994 (first entry)
DT	Murine Fas.
DE	Murine Fas.
KW	Murine; Fas; human; macrophage; cell strain; BAM3.
XX	Mus musculus.
OS	JP05219959-A.
PN	31-AUG-1993.
XX	14-FEB-1992; 92JJP-0028090.
XX	14-FEB-1992; 92JJP-0028090.
XX	(OSAB-) 2H OSAKA BIOSCIENCE KENKYUSHO.
XX	WPI; 1993-308326/39.
DR	N-PSDB; AAQ48008.
XX	DNA hybridising with sequence coding for human Fas protein - is
PT	prepd. from e.g. BAM3 cell of mouse macrophage cell
XX	Claim 1; Page 6-7; 8pp; Japanese.
PS	This sequence represents the murine Fas protein. The cDNA encoding
XX	
CC	

CC this sequence hybridises with the human Fas gene and was isolated
CC from the mouse macrophage cell strain BAM3. This sequence may be
CC used for the production of large amounts of murine Fas.

XX Sequence 327 AA;

Query Match 100.0%; Score 1804; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.1e-140;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCCQPCQ 60
DB 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCCQPCQ 60
QY 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
DB 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
QY 121 TKCKCKPDFYCDSPGCEHCVRASCCEHGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
DB 121 TKCKCKPDFYCDSPGCEHCVRASCCEHGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
QY 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPIRIADMTIOEAKKF 240
DB 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPIRIADMTIOEAKKF 240
QY 241 ARENNIKEGIDETIMHDSIQDTAEQKVQLLWCYQSHGKSDAYQDLIKGLKKAECRTILD 300
DB 241 ARENNIKEGIDETIMHDSIQDTAEQKVQLLWCYQSHGKSDAYQDLIKGLKKAECRTILD 300
QY 301 KFQDMVQKDLGKSTPDTGNEGQCLE 327
DB 301 KFQDMVQKDLGKSTPDTGNEGQCLE 327

RESULT 2

AAR78611
ID AAR78611 standard; Protein; 327 AA.

XX AAR78611;

XX 19-FEB-1996 (first entry)

XX Murine Fas antigen extracellular region.

XX Murine Fas antigen; extracellular region; soluble membrane protein;
KW antibody production; diseases; treatment; prevention.

XX Mus musculus.

XX Key Location/Qualifiers
FH Peptide 1..21
FT Peptide /label= sig_peptide
FT Peptide 22..327
FT Peptide /label= mat_peptide

XX JP07115988-A.

XX 09-MAY-1995.

XX 26-OCT-1993; 93JP-0267644.

XX 26-OCT-1993; 93JP-0267644.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 1995-202847/27.

XX N-PSDB; AAQ95302.

XX Preparation of soluble membrane proteins - for their use in antibody
PT production for the treatment and prevention of related diseases

XX Example 2; Pages 32-33; 51pp; Japanese.

XX

CC AAQ95302 encodes AAR78611 the murine Fas antigen extracellular region.
CC The cDNA was used in the construction of an expression vector for
CC the prodn. of recombinant soluble membrane proteins. The proteins
CC can be used in antibody prodn. for the treatment and prevention of
CC related diseases.

XX Sequence 327 AA;

Query Match 100.0%; Score 1804; DB 16; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.1e-140;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCCQPCQ 60
DB 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCCQPCQ 60
QY 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
DB 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
QY 121 TKCKCKPDFYCDSPGCEHCVRASCCEHGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
DB 121 TKCKCKPDFYCDSPGCEHCVRASCCEHGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
QY 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPIRIADMTIOEAKKF 240
DB 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPIRIADMTIOEAKKF 240
QY 241 ARENNIKEGIDETIMHDSIQDTAEQKVQLLWCYQSHGKSDAYQDLIKGLKKAECRTILD 300
DB 241 ARENNIKEGIDETIMHDSIQDTAEQKVQLLWCYQSHGKSDAYQDLIKGLKKAECRTILD 300
QY 301 KFQDMVQKDLGKSTPDTGNEGQCLE 327
DB 301 KFQDMVQKDLGKSTPDTGNEGQCLE 327

RESULT 3

AAR92530
ID AAR92530 standard; Protein; 327 AA.

XX AAR92530;

XX 06-SEP-1996 (first entry)

XX mFas sequence.

XX Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW rheumatoid arthritis; serum; systemic lupus erythematosus.

XX Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..21
FT Peptide /note= "signal peptide"
FT Protein 22..327
FT Misc-difference 24 /note= "mature Fas"
FT /note= "encoded by AGT"

XX WO9601277-A1.

XX 18-JAN-1996.

XX 03-MAR-1995; 95WO-JP00349.

XX 14-FEB-1995; 95JP-0025637.

XX 06-JUL-1994; 94JP-0154706.

XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA (NISB) JAPAN TOBACCO INC.

XX

PI Hachiya T, Noguchi J, Yonehara S;
 XX WPI: 1996-087635/09.
 DR N-PSDB; AAT16305.
 XX
 XX Immunoassay method for soluble Fas antigen in body fluids - for
 PT diagnosis of autoimmune diseases such as rheumatoid arthritis and
 PT systemic lupus erythematosus
 XX
 XX Example 9; Page 80-82; 124pp; Japanese.
 PS
 XX This sequence represents the mFas antigen used for the mFas.EXT,
 CC contained within the plasmid pME18S. The soluble Fas antigen is included
 CC in the immunoassay kit of the invention. The kit is for the assay of
 CC soluble Fas antigen and contains an immobilised anti-soluble Fas
 CC monoclonal antibody, as well as the standard soluble Fas antigen
 CC represented by this sequence. The assay is simple and has high accuracy,
 CC high sensitivity, and is capable of assaying a number of different
 CC specimens at the same time. The immunoassay is used on biological
 CC samples (such as serum) and is useful for diagnosis of autoimmune
 CC diseases such as rheumatoid arthritis or systemic lupus erythematosus
 CC (SLE).
 XX
 SQ Sequence 327 AA;
 Query Match 100.0%; Score 1804; DB 17; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.1e-140;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 DB 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 QY 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 DB 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 QY 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTILVLLI 180
 DB 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTILVLLI 180
 QY 181 PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSSKYIPRIAEDMTIOEAKKF 240
 DB 181 PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSSKYIPRIAEDMTIOEAKKF 240
 QY 241 ARENNIEGKIDEIMHDSIQDTAEQKVOLLCWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 DB 241 ARENNIEGKIDEIMHDSIQDTAEQKVOLLCWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 QY 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 DB 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 RESULT 4
 AAB19344
 ID AAB19344 standard; Protein: 327 AA.
 XX
 AC AAB19344;
 XX
 XX 06-MAR-2001 (first entry)
 DT
 XX Amino acid sequence of a murine Fas (Apo-1) protein.
 DE
 XX Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
 KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
 KW autoimmune disease; inflammatory disease; lymphoma.
 XX
 OS Mus musculus.
 XX
 XX W0200061150-A1.
 PN
 XX 19-OCT-2000.
 PD

XX 10-APR-2000; 2000WO-US09540.
 PF
 XX 12-APR-1999; 99US-0290640.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Dean NM, Marcussen EG;
 PI
 XX WPI: 2000-628395/60.
 DR
 DR N-PSDB; AAC61859.
 XX
 PT Antisense oligonucleotides for treating hepatitis and colon, liver or
 PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
 PT 1 (Fap-1) expression
 XX
 XX Example 5; Page 108-109; 116pp; English.
 PS
 XX The present sequence represents murine Fas (Apo-1). The specification
 CC describes antisense compounds which are targeted to the 5'-untranslated
 CC region, translational start site, translational termination region
 CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
 CC ligand (FasL), or Fap-1 (Fas associated protein.1, protein tyrosine
 CC phosphatase). The antisense compounds are used to inhibit the
 CC expression of Fas, FasL or Fap-1 in cells or tissues. They are used
 CC to treat autoimmune or inflammatory diseases such as hepatitis. They
 CC can also be used to treat cancer, especially colon, liver or lung
 CC cancer or lymphoma.
 XX
 SQ Sequence 327 AA;
 Query Match 100.0%; Score 1804; DB 21; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.1e-140;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 DB 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 QY 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 DB 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 QY 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTILVLLI 180
 DB 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTILVLLI 180
 QY 181 PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSSKYIPRIAEDMTIOEAKKF 240
 DB 181 PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSSKYIPRIAEDMTIOEAKKF 240
 QY 241 ARENNIEGKIDEIMHDSIQDTAEQKVOLLCWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 DB 241 ARENNIEGKIDEIMHDSIQDTAEQKVOLLCWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 QY 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 DB 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 RESULT 5
 AAW86241
 ID AAW86241 standard; Protein: 327 AA.
 XX
 AC AAW86241;
 XX
 XX 16-FEB-1999 (first entry)
 DT
 XX Fas ligand (FasL) protein.
 XX
 XX Fas ligand; FasL; Fas receptor; tumour; non-tumourigenic; T cell;
 KW rhabdomyosarcoma; killing; myoblast cell; immune provocation;
 KW neutrophil; detection.

KW	antibody production; diseases; treatment; prevention.
XX	Synthetic.
OS	
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..21
FT	/label= sig_peptide
FT	22..169
FT	/label= mat_peptide
XX	
XX	JP07115988-A:
PN	
XX	
PD	09-MAY-1995.
XX	
XX	26-OCT-1993; 93JP-0267644.
PF	
XX	
PR	26-OCT-1993; 93JP-0267644.
XX	
PA	(NISR) JAPAN TOBACCO INC.
XX	
DR	WPI; 1995-202847/27.
DR	N-PSDB; AAQ95305.
XX	
PT	Preparation of soluble membrane proteins - for their use in antibody
PT	production for the treatment and prevention of related diseases
XX	
XX	Example 2; Pages 34-35; 51pp; Japanese.
CC	AAQ95305 is the plasmid fragment pM18S which encodes AAR78612. The
CC	plasmid was used in the construction of an expression vector for
CC	the prodn. of recombinant soluble membrane proteins. The proteins
CC	can be used in antibody prodn. for the treatment and prevention of
CC	related diseases.
XX	
SQ	Sequence 169 AA;
Query Match	54.2%; Score 977; DB 16; Length 169;
Best Local Similarity	100.0%; Pred. NO. 1.7e-72;
Matches 169; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MLWTWAVLPLVLAGSQLRVHTQTGNTSISLSKLRVRVHETDKNCSEGLYQGPGFCCPCQ 60
DB	1 MLWTWAVLPLVLAGSQLRVHTQTGNTSISLSKLRVRVHETDKNCSEGLYQGPGFCCPCQ 60
QY	61 PGKKVKEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRTLCDEHGLEVETNCTLTQN 120
DB	61 PGKKVKEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRTLCDEHGLEVETNCTLTQN 120
QY	121 TKCKCKPDFYCDSFGCEHCVCASCEHGTLEPCTATSTNCRKQSPNR 169
DB	121 TKCKCKPDFYCDSFGCEHCVCASCEHGTLEPCTATSTNCRKQSPNR 169
RESULT 9	
AAM64484	
ID	AAM644484 standard; Protein; 669 AA.
XX	
XX	AAM64484;
XX	
DT	20-OCT-1998 (first entry)
XX	
DE	Human TNFR1 protein.
XX	
KW	Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation;
KW	agonist; tumour necrosis factor; TNF; ligand; autoimmune disease;
KW	infection; graft rejection; antagonist; inhibitor; diagnostic.
XX	
OS	Homo sapiens.
XX	
PN	WO9832856-A1.
XX	
PD	30-JUL-1998.
XX	

[illegible]

[illegible]

RESULT 13	
AAR92528	
ID	AAR92528 standard; Protein; 335 AA.
XX	
XX	AAR92528;
AC	
XX	
XX	
DT	06-SEP-1996 (first entry)
XX	
DE	hFas from plasmid pCEV4/hFas.
DE	
XX	
XX	
KW	Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW	rheumatoid arthritis; serum; systemic lupus erythematosus.
XX	
OS	Synthetic.

PH	Key	Location/Qualifiers
FT	Peptide	1..16
FT		/note= "hFas signal peptide"
FT	Protein	17..335
FT		/note= "mature hFas"
XX		
XX	W09601277-A1.	
XX		
XX		
PD	18-JAN-1996.	
XX		
XX	03-MAR-1995;	95WO-JP00349.
XX		
XX	14-FEB-1995;	95JP-0025637.
PR		
PR	06-JUL-1994;	94JP-0154706.
XX		
XX		
PA	(MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.	
PA	(NISB) JAPAN TOBACCO INC.	
XX		
XX		
PI	Hachiya T, Noguchi J, Yonehara S;	
XX		
DR	WPI; 1996-087635/09.	
DR	N-PSDB; AAT16303.	

Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto-immune diseases such as rheumatoid arthritis and systemic lupus erythematosus

Example 8; Page 49-52; 124pp; Japanese.

CCC This sequence represents the sequence for the human Fas antigen contained within the plasmid pCEV4/hFas. The soluble Fas antigen is included in

the immunoassay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas monoclonal antibody, as well as the standard soluble Fas antigen represented by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus (SLE).

Sequence 335 AA;

Query Match	47.5%	Score 856;	DB 17;	Length 335;
Best Local Similarity	49.4%	Pred. No. 3.4e-62;		
Matches 165;	Conservative 54;	Mismatches 107;	Indels 8;	Gaps 3
QY	1	MLWIAVPLVLVAG----	SQLRVHQGTGNSISLKLRRRVHETKNCSEGLYQGGPFCC	56
Db	1	MLGIWTLPLVLVTSVARLSSKSVNAQVTDINSKGLELRKTVTVETQNLGHHDDQGFCH	60	
QY	57	QPCOPGKKVDECKMNGTPTCAPCTEGEKYMDKNHYADKRCRCLTCDEHGLEVEYNCT	116	
Db	61	KPCPPGKAKDCITVNGDEPPCVPQCGKEYTDKAHFSKCRRCRLCDEGHGLEVEYNCT	120	

[illegible]

RESULT 14
AAW50289
ID AAW50289 standard; Protein; 335 AA.
XX
AC AAW50289;

DT 16-JUL-1998 (first entry)

Human Fas antigen.

Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV; apoptosis modulation.

XX
OS
Homo sapiens.

XX	Key	Location/Qualifiers
FH	Peptide	1..16
FT		

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FT      /label= sig_peptide  
FT      17..335  
FT      /label= mat_peptide
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FT	Region
17..173	/note= "claimed fragment"

WO9742319-A1.

13-NOV-1997

01-MAY-1967

[illegible]

XX
20 OCT 1950, 1000Z
300F-0133/60.

PA (MOCH) MOCHIDA PHARM CO LTD.
XX (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N;
XX WPI; 1997-558981/51.
DR N-PSDB; AAV07002.
XX Fas antigen derivative containing modified extracellular region -
PT has low antigenicity, promotes apoptosis and is useful in treatment
PT of viral and other diseases
XX Claim 2; Fig 1-2; 102pp; Japanese.
XX The present sequence was used in the development of novel Fas
CC antigen derivatives, which contain a Fas antigen extracellular
CC region lacking one or more amino acid residues in the region from
CC the amino-terminal to (but excluding) the 1st cysteine residue
CC (preferably at least 29 residues are deleted).
CC The derivatives are effective regulators of apoptosis and can be
CC used (either by administration of the polypeptide, or by the use
CC of the coding DNA in gene therapy) to treat a range of diseases,
CC e.g. diabetes, arthritis, lupus and in particular viral diseases
CC such as hepatitis, influenza and HIV, by modulating apoptosis of
CC virus-infected cells.
XX
SQ Sequence 335 AA;
Query Match 47.5%; Score 856; DB 18; Length 335;
Best Local Similarity 49.4%; Pred. No. 3.4e-62;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLWTWAVLPLVLG---SQLRVHTQGTNSISESLKLRVRYHENDKNCSEGLYGGPFCC 56
DB 1 MLGWTLLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 57 QPCPGKRVKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 61 KPCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDDEHGLEVEINCT 120
QY 117 LTQNTKCKKPDYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPNRNLLTIL 176
DB 121 RTQNTKCRKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNCKEGRSRLGLWCLL 180
QY 177 VLLIPL-VFIYKRYKRRKCKRRDDP---ESRTSSRTIPWNASNLSLYIPRIADM 232
DB 181 LLPIPLIWWKKEVQKTCRKHENQGSHPILNPTVAINLSVDVLSKYIITIAVM 240
QY 233 TIQBAKFARNNIKEGKIDIMHDSIQDTAEQKVQLLLCWYQSHGSKSDAYQDLIKGLK 292
DB 241 TLSQVKGVRKNGVNEAKIDEKNDVQDTAEQKVQLLRNHLHKGKAYDTLIKDLK 300
QY 293 AECRTLDKFQDMVKLGKSTPDTGNEGQCL 326
DB 301 ANCLTAEKIQTILKIDTSDSENSFNRIQSL 334
RESULT 15
AAW49104
ID AAW49104 standard; Protein; 335 AA.
XX
AC AAW49104;
XX
DT 18-NOV-1998 (first entry)
XX
DE Fas protein.
XX Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
KW simian immunodeficiency virus; HIV; cytotoxic T lymphocyte; CTL;
XX prophylactic; AIDS.
OS Mammalia sp.

XX Key Location/Qualifiers
FH Peptide 1..16
FT /note= "Signal peptide"
FT Protein 17..335
FT /note= "Fas protein"
FT Region 17..172
FT /note= "The portion of a Fas protein which can be
FT fused to a Fc polypeptide to form a Fas-Fc
FT fusion protein"
XX
PN WO9835692-A1.
XX
XX 20-AUG-1998.
XX
XX 17-FEB-1998; 98WO-GB00485.
XX
XX 17-FEB-1997; 97GB-0003276.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Screaton GR, Xu X;
XX
XX WPI; 1998-456867/39.
XX
XX N-PSDB; AAV32993.
XX
XX Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
XX diseases - by interfering with interaction of Fas with Fas-ligand
XX expressed on activated CD4+ cells, e.g. cells infected with HIV
XX Disclosure; Fig 7; 71pp; English.
XX
XX The present sequence represents a Fas protein sequence used in the
XX method of the invention. The method is concerned with reducing
XX depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
XX cells in an immune cell population which also comprises of Fas-ligand
XX (FasL)-expressing activated CD4+ cells. It involves contacting this
XX immune cell population with an effective amount of an agent (e.g. a
XX soluble Fas-Fc fusion protein) which would interfere with the
XX interaction between Fas and FasL. Therefore, the method is useful for
XX identifying suitable agents which can reduce depletion of activated
XX Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
XX is the use of the agent in the manufacture of therapeutic compositions.
XX Apoptosis of lymphocytes can be triggered by the interaction of the
XX cell surface receptor Fas and its ligand FasL. By interfering with
XX this interaction, the method described and its preparations can prevent
XX apoptosis of CD8+ TK lymphocytes caused by its expression of FasL on
XX activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
XX especially the result of CD4+ cell infection with an immunodeficiency
XX virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
XX virus (SIV). The claimed prevention of apoptosis may then allow
XX maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
XX towards the CD4+ cells infected with the infectious agent, enabling
XX treatment (prophylactic and/or therapeutic) of immunodeficiency
XX diseases e.g. AIDS.
SQ Sequence 335 AA;
Query Match 47.5%; Score 856; DB 19; Length 335;
Best Local Similarity 49.4%; Pred. No. 3.4e-62;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLWTWAVLPLVLG---SQLRVHTQGTNSISESLKLRVRYHENDKNCSEGLYGGPFCC 56
DB 1 MLGWTLLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 57 QPCPGKRVKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 61 KPCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDDEHGLEVEINCT 120
QY 117 LTQNTKCKKPDYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPNRNLLTIL 176
DB 121 RTQNTKCRKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNCKEGRSRLGLWCLL 180

Search completed: May 9, 2003, 17:05:11
Job time : 61.3354 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 17:03:26 ; Search time 12.8429 seconds
(without alignments)
749.153 Million cell updates/sec

Title: US-09-446-634A-23
Perfect score: 1804
Sequence: 1 MLWIWAVLPLVLGSQLRVH.....KDLGKSTPDGTGNEGOCLE 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	327	US-09-290-640-66	Sequence 66, Appl
2	863.5	47.9	669	US-09-013-895A-3	Sequence 3, Appl
3	863.5	47.9	669	US-09-448-868-3	Sequence 3, Appl
4	856	47.5	335	US-08-219-237B-2	Sequence 2, Appl
5	856	47.5	335	US-08-409-338-1	Sequence 1, Appl
6	856	47.5	335	US-09-290-640-2	Sequence 2, Appl
7	856	47.5	335	US-09-006-353A-7	Sequence 7, Appl
8	856	47.5	335	US-08-468-560C-2	Sequence 2, Appl
9	856	47.5	335	US-09-180-100-20	Sequence 20, Appl
10	856	47.5	335	US-09-565-918-3	Sequence 3, Appl
11	856	47.5	335	US-09-573-986-7	Sequence 7, Appl
12	856	47.5	335	PCT-US95-17083-2	Sequence 2, Appl
13	844	46.8	335	US-08-815-469-6	Sequence 6, Appl
14	825	45.7	331	US-09-086-483A-3	Sequence 3, Appl
15	810.5	44.9	314	US-08-444-231-19	Sequence 19, Appl
16	810.5	44.9	314	PCT-US95-17083-4	Sequence 4, Appl
17	810.5	44.9	314	US-09-527-236A-3	Sequence 3, Appl
18	645	35.8	281	US-08-974-022-45	Sequence 45, Appl
19	585	32.4	219	US-08-795-445A-45	Sequence 45, Appl
20	585	32.4	219	US-08-795-447A-45	Sequence 45, Appl
21	585	32.4	219	US-08-974-186-45	Sequence 45, Appl
22	585	32.4	219	US-08-795-446B-45	Sequence 45, Appl
23	585	32.4	219	US-08-706-945D-131	Sequence 131, Appl
24	585	32.4	219	US-08-828-683A-22	Sequence 22, Appl
25	523	29.0	167	US-09-180-100-15	Sequence 15, Appl
26	496	27.5	157	US-09-180-100-15	Sequence 15, Appl
27	494.5	27.4	144	US-09-180-100-21	Sequence 21, Appl

28	494.5	27.4	159	4	US-09-180-100-23	Sequence 23, Appl
29	494.5	27.4	376	4	US-09-180-100-22	Sequence 22, Appl
30	470	26.1	128	4	US-09-180-100-9	Sequence 9, Appl
31	470	26.1	143	4	US-09-180-100-10	Sequence 10, Appl
32	470	26.1	360	4	US-09-180-100-11	Sequence 11, Appl
33	462	25.6	119	4	US-08-828-683A-15	Sequence 15, Appl
34	460	25.5	119	2	US-08-219-237B-3	Sequence 3, Appl
35	460	25.5	119	4	US-08-477-347-14	Sequence 14, Appl
36	460	25.5	119	4	US-08-476-862-5	Sequence 5, Appl
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38	305.5	16.9	149	5	PCT-US95-17083-6	Sequence 6, Appl
39	230	12.7	85	4	US-09-042-785A-26	Sequence 26, Appl
40	218	12.1	41	1	US-08-444-005-32	Sequence 32, Appl
41	215	11.9	468	4	US-09-013-895A-2	Sequence 2, Appl
42	215	11.9	468	4	US-09-565-918-2	Sequence 2, Appl
43	215	11.9	468	4	US-09-448-868-2	Sequence 2, Appl
44	214	11.9	40	1	US-08-444-005-26	Sequence 26, Appl
45	210.5	11.7	467	4	US-09-086-483A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-290-640-66
; Sequence 66, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290.640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-290-640-66
Query Match 100.0%; Score 1804; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 6.7e-158;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLWIWAVLPLVLGSQLRVHQTGNTSISLSKLRRRVHETDKNCSEGLYQGPFCCQPCQ	60
Db	1	MLWIWAVLPLVLGSQLRVHQTGNTSISLSKLRRRVHETDKNCSEGLYQGPFCCQPCQ	60
Qy	61	PGKKVEDCKMNGSTPCAPCTEGKEYMDKNHYADKRCRTLCDEHGLEVTNCTLTQN	120
Db	61	PGKKVEDCKMNGSTPCAPCTEGKEYMDKNHYADKRCRTLCDEHGLEVTNCTLTQN	120
Qy	121	TKCKCKDFYCDSPGCEHVCRCASCEHGTLEPCTATSNCRKQSPRNLRLWLLTLVL	180
Db	121	TKCKCKDFYCDSPGCEHVCRCASCEHGTLEPCTATSNCRKQSPRNLRLWLLTLVL	180
Qy	181	PLVFYFYRKRKCKWKRRQDDPESRTSRETIPMNASNLSSKYIPRTAEDMTIQEAKKF	240
Db	181	PLVFYFYRKRKCKWKRRQDDPESRTSRETIPMNASNLSSKYIPRTAEDMTIQEAKKF	240
Qy	241	ARENNIKEGKIDEIMHDSITQDTAEQVQLLCLWYQSHGKSDAYQDLIKGLKKAECRR	300
Db	241	ARENNIKEGKIDEIMHDSITQDTAEQVQLLCLWYQSHGKSDAYQDLIKGLKKAECRR	300
Qy	301	KFQDMVQKDLGKSTPDGTGNEGOCLE	327
Db	301	KFQDMVQKDLGKSTPDGTGNEGOCLE	327

RESULT 2
US-09-013-895A-3

Sequence 3, Application US/09013895A
Patent No. 6342363
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013.895A
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-013-895A-3

Query Match 47.9%; Score 863.5; DB 4; Length 669;
Best Local Similarity 49.2%; Pred. No. 4.2e-71;
Matches 164; Conservative 54; Mismatches 108; Indels 7; Gaps 2;
QY 1 MLWIAVLPVLAG----SOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYOGGPFCC 395
Db 336 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVTVTONLEGLHHDGQFCH 395
QY 57 QPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 396 KCPGPKRKARDCTVNGDEPDCVPCQEGREYTDKAHFSKRCRCRLCDDEHGLEVEINCT 455
QY 117 LTQNTKCKKPFYCDSPGCEHCVCASCHEGTLEPCTATSNTRCNKQSPRNLWLTL 176
Db 456 RTQNTKRCCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRNLGLWCLL 515
QY 177 VLLIPLVLYRYKRRKCKWRQDDP---ESRTSSRETIPMNASLNSKYIPRIAEWMT 233
Db 516 LLPIPLVYKREVKQTKRHKRKNQSGHESPTLPETVAINLSDVLSKYITTIAGVMT 575
QY 234 IQEAKKFARENKKEGKIDEIMHDSIQDTAEQVOLLCLCWYQSHGSKSDAYDLKGLKKA 293
Db 576 LSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHLGKKEAYDTLIDKLKKA 635
QY 294 ECRRTLDKQDMVQDKLGKSTPDTGNENEGQL 326
Db 636 NLCTLAETIQLIDKITSDSNENRNEIQSL 668

RESULT 3
US-09-448-868-3
Sequence 3, Application US/09448868
Patent No. 6461823
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448.868
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013.895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-868-3

Query Match 47.9%; Score 863.5; DB 4; Length 669;
Best Local Similarity 49.2%; Pred. No. 4.2e-71;
Matches 164; Conservative 54; Mismatches 108; Indels 7; Gaps 2;
QY 1 MLWIAVLPVLAG----SOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYOGGPFCC 395
Db 336 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVTVTONLEGLHHDGQFCH 395
QY 57 QPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 396 KCPGPKRKARDCTVNGDEPDCVPCQEGREYTDKAHFSKRCRCRLCDDEHGLEVEINCT 455
QY 117 LTQNTKCKKPFYCDSPGCEHCVCASCHEGTLEPCTATSNTRCNKQSPRNLWLTL 176
Db 456 RTQNTKRCCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRNLGLWCLL 515
QY 177 VLLIPLVLYRYKRRKCKWRQDDP---ESRTSSRETIPMNASLNSKYIPRIAEWMT 233
Db 516 LLPIPLVYKREVKQTKRHKRKNQSGHESPTLPETVAINLSDVLSKYITTIAGVMT 575
QY 234 IQEAKKFARENKKEGKIDEIMHDSIQDTAEQVOLLCLCWYQSHGSKSDAYDLKGLKKA 293
Db 576 LSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHLGKKEAYDTLIDKLKKA 635


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QY 177 VLLIPL-VFIYKRYKRCMKRRDDP- --ESRTSSRETIPNMASNLISKYIPRIADM 232
Db 181 LLIPLIIVWVRKKEVQKTCRKHKEGSGHESPTLNPETVAINLSVDVLSKVTITTIAGVM 240
QY 233 TIOEAKKFARENNNIKEGKIDEIMHDSIQDTAEQKVOVLKLCWYQSHGSDAYODLKGCLK 292
Db 241 TILSQVGKGVRRKGVNEAKIDEIKNDNVQDTAEQKVOILLRNWHLQHGKKEAVDTLKLKCLK 300
QY 293 AECRRITDKDFQDMQKDLGKSTPDTGNEEGQCL 326
Db 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIQSL 334

RESULT 6
US-09-290-640-2
; Sequence 2, Application US/09290640
; Patent No. 620405
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-290-640-2

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[illegible]

RESULT 7
US-09-006-353A-7
; Sequence 7, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
;

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-006-353A-7

```

Query Match      47.5%; Score 856; DB 4; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3

```

QY	1	MLMTWAVLPVLAG-----SQRVHTQTGNISSESUKLRRRVRHETDKNCGSEGLYQGCPGCC	56
DB	1	MLGWLTPPLVLTSVARLUSSVAQAQVTDINSKGLELRKTVTTVETQNLEGLHHGDQFCH	60
QY	57	QPCQPGKKKBEDCKRMNGGTPTCAPCTEGEKYMDKNHYADKCRCRTCLCDEEHGLEVETNCT	116
DB	61	KPCPPGERKARDCTVNGDEPDPCVCQEGKEYTDAHFSSSKRCRCRLCDCEHGHEVEINCT	120
QY	117	LTONTKCKCRPDFCYDSPGCBCVRCASCEHGTLEPCTATSNTRKQSPRNRLWWLLTL	176
DB	121	RTQNTKCRCPNFECSTVCEHCDCPTCKEHIKECTLTSTNKCKEGRSNNLGWLCLL	180
QY	177	VLIAPLVFYTRYKYRKXKWKRRODDP---ESRTSSRETTIPMAASNLSKYIPRIADM	232
DB	181	LLPILPVWVKREVQTCRKHKENOGSHESP LNPTVAINLSDVLSKYITTIAGVM	240
QY	233	TIOEAKKFARENNIKEGIDIEIMHDSIQDTAEOKVOLLLCWYOSHGGSKDAYQDLIKGLK	292
DB	241	TLSQLVGKGVKNGVNEAKIDEINKDNVDPTAEOKVOLLNRNHQLHGKKEAYDTLIIRLKK	300
QY	293	AECERTILDKFDWMQVKDLGKSTPDTGNENBGQCL	326
DB	301	ANUCLTAELKIOTIILKDITSDSNSFNFRNIOSL	334

RESULT 8
 US-08-468-560C-2
 ; Sequence 2, Application US/08468560C
 ; Patent No. 6270998
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGATA, Shigekazu
 ; APPLICANT: ITOH, Naoto
 ; APPLICANT: YONEHARA, Shin
 ; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
 ; TITLE OF INVENTION: ANTIGEN
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.


```

QY 57 QPCPGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKCRCTCLCDEHGLEVEINCT 116
Db 61 KPCPPGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKCRRCRLCDEHGLEVEINCT 120
QY 117 LTQNTCKCKPDPYCDSPGCEHCVCRCASCEHGTLEPCTATNTNCRKQSPRNLWLLTIL 176
Db 121 RTQNTCKCRCKPNFNCSTVCEHCDPCTCKEHIKECTILTSNTKCKEGRSRLGLWLCUL 180
QY 177 VLLIPL-VFIYKRYKRCWKRRQDDP---ESRTSSRETIPMNASLNSKYIPRIADM 232
Db 181 LLIPLIIVWVKRQVQKTCRKRRKNOGSHESPTLNPTVAINLSDVLSKYITTIAGVM 240
QY 233 TIOEAKKFARENNIKEGKIDETIMHDSIODTAQKQVOLLICWYQSHGKSDAYQDLIKGLKK 292
Db 241 TLSQVKGFRKNGVNEAKIDEKNDVQDTAEQVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 293 AECRTLQKFDQVMDKLGKSPDPTGNEGQCL 326
Db 301 ANLCTLAEKIQTILKIDTSSENSNFRNEIQSL 334

RESULT 11
US-09-573-986-7
; Sequence 7, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-7

Query Match 47.5%; Score 856; DB 4; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWAVLPLVLG----SOLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGGPFCC 56
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCPGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKCRCTCLCDEHGLEVEINCT 116
Db 61 KPCPPGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKCRRCRLCDEHGLEVEINCT 120
QY 117 LTQNTCKCKPDPYCDSPGCEHCVCRCASCEHGTLEPCTATNTNCRKQSPRNLWLLTIL 176
Db 121 RTQNTCKCRCKPNFNCSTVCEHCDPCTCKEHIKECTILTSNTKCKEGRSRLGLWLCUL 180
QY 177 VLLIPL-VFIYKRYKRCWKRRQDDP---ESRTSSRETIPMNASLNSKYIPRIADM 232
Db 181 LLIPLIIVWVKRQVQKTCRKRRKNOGSHESPTLNPTVAINLSDVLSKYITTIAGVM 240
QY 233 TIOEAKKFARENNIKEGKIDETIMHDSIODTAQKQVOLLICWYQSHGKSDAYQDLIKGLKK 292
Db 241 TLSQVKGFRKNGVNEAKIDEKNDVQDTAEQVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 293 AECRTLQKFDQVMDKLGKSPDPTGNEGQCL 326
Db 301 ANLCTLAEKIQTILKIDTSSENSNFRNEIQSL 334

RESULT 12
US-09-573-986-7
; Sequence 7, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-7

Query Match 47.5%; Score 856; DB 4; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWAVLPLVLG----SOLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGGPFCC 56
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCPGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKCRCTCLCDEHGLEVEINCT 116
Db 61 KPCPPGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKCRRCRLCDEHGLEVEINCT 120
QY 117 LTQNTCKCKPDPYCDSPGCEHCVCRCASCEHGTLEPCTATNTNCRKQSPRNLWLLTIL 176
Db 121 RTQNTCKCRCKPNFNCSTVCEHCDPCTCKEHIKECTILTSNTKCKEGRSRLGLWLCUL 180
QY 177 VLLIPL-VFIYKRYKRCWKRRQDDP---ESRTSSRETIPMNASLNSKYIPRIADM 232
Db 181 LLIPLIIVWVKRQVQKTCRKRRKNOGSHESPTLNPTVAINLSDVLSKYITTIAGVM 240
QY 233 TIOEAKKFARENNIKEGKIDETIMHDSIODTAQKQVOLLICWYQSHGKSDAYQDLIKGLKK 292
Db 241 TLSQVKGFRKNGVNEAKIDEKNDVQDTAEQVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 293 AECRTLQKFDQVMDKLGKSPDPTGNEGQCL 326
Db 301 ANLCTLAEKIQTILKIDTSSENSNFRNEIQSL 334

RESULT 13
US-08-815-469-6
; Sequence 6, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-815-469-6

Query Match 46.8%; Score 844; DB 4; Length 335;
Best Local Similarity 49.1%; Pred. No. 1.1e-69;
Matches 164; Conservative 54; Mismatches 108; Indels 8; Gaps 3;

QY 1 MLWTAVLPLVLG----SQLRVHTQGTNSISESLKRRRHVETDKNCSEGLYQGPFCC 56
DB 1 MGLTWLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 57 QPCPGKKKVEDCKNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHLEVEINCT 120
QY 117 LTQNTKCKCPDFCYDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRLLWLTIL 176
DB 121 RTQNTKCKCPNFQNTVCEHCDPCTKCEHGIIECTLTNTNCRKEGSRNLGLWCLL 180
QY 177 VLLIPL-VFIYKRYKRRKCRKRRDDP---ESRTSSRETIPMNASNLISKYIPRIADM 232
DB 181 LLPIPLIWWKRVKQKTCRKRKENQSGHESPTLNPTVAINLSDVDLSKYITTIAGVM 240
QY 233 TIOEAKKFARENNKEGKIDEIMHDSIQDTAEQKVQLLWCYQSHGKSDAYODLIKGLKK 292
DB 241 TLSQVKGFEVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
QY 293 AECRRLDKFQDMVKDGLKSTPDTGNENEGQCL 326
DB 301 ANLCTLAETKIITLKDITSDSENSNFRNEIQSL 334

RESULT 14
US-08-815-469-6
Sequence 3, Application US/09086483A
Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/086,483A
APPLICATION NUMBER: 60/050,936
FILING DATE: May-30-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-086-483A-3

Query Match 45.7%; Score 825; DB 4; Length 331;
Best Local Similarity 49.9%; Pred. No. 5.7e-68;
Matches 167; Conservative 53; Mismatches 101; Indels 14; Gaps 8;

QY 1 MLWTAVLPLVLG----SQLRVHTQGTNSISESLKRRRHVETDKNCSEGLYQGPFCC 56
DB 1 MGLTWLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNL-EGLRHGQF-C 58
QY 57 QPCPGKKKVEDCKNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 59 HPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHLEVEINCT 118
QY 117 LTQNTKCKCPDFCYDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRLLWLTIL 176
DB 119 RTQNTKCKCPNFQNTVCEHCDPCTKCEHGIIECTLTNTNCRKEGSRNGL-LCLL 177
QY 177 VLLIPL-VFIYKRYKRRKCRKRRDDP---ESRTSSRETIPMNASNLISKYIPRIADM 232
DB 178 LLPIPLIWWKRVKQKTCRKRKENQSGHESPTLNPTVAINLSDVDLSKYITTIAGVM 237
QY 233 TIOEAKKFARENNKEGKIDEIMHDSIQDTAEQKVQLLWCYQSHGKSDAYODLIKGLKK 292
DB 238 TLSQVKGFEVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 297
QY 293 AE-CRRTLDKFDQDMVKDGLKSTPDTGNENEGQCL 326
DB 298 ANLC--TLAETKIITLKDITSDSENSNFRNEIQSL 330

RESULT 15
US-08-444-231-19
Sequence 19, Application US/08444231
Patent No. 5652210
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-231-19

Query Match 44.9%; Score 810.5; DB 1; Length 314;
Best Local Similarity 46.8%; Pred. No. 1.2e-66;
Matches 156; Conservative 50; Mismatches 100; Indels 27; Gaps 3;
QY 1 MLWIWVLPVLAG-----SOLRVHTQNTSISBSLKLRRRVHETDKNCSEGLYQGGPFCC 56
Db 1 MLGIWTLPLVLT/SVARLSSKSVNAQVTDINSKGLERKVTVTVEITONLESLHHDGQFCH 60
QY 57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCCTLCDEHGLEVEINCT 116
Db 61 KPCPPGERKARDCTVNGDEPCVQEGKEYTDKAHFSSKRCRCRLCDEHGLEVEINCT 120
QY 117 LTQNTCKCKPDCYDPCGCEHCVCASCCEHGTLEPCTATSNCRKQSPRNLWLLTIL 176
Db 121 RTQNTKRCCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNFKCEE----- 168
QY 177 VLIPLVFIYKRYKRCCKWRRODDP---ESRTSSRETIPMNASNLISKYIPRIAE DMT 233
Db 169 -----VKREVKQTCRKHRENQGSHPETLNPETVAINLSDVDLSKYITTIAGVMT 220
QY 234 IQEAKFARENKKEGKIDTAEQKQVQLLWYQSHGSKSDAYQDLIKLKA 293
Db 221 LSQVKGFRKNGVNEAKIDEIKNDVQAEQKQVQLLWYQSHGSKSDAYQDLIKLKA 280
QY 294 ECRRTLDKFQDMVQDLGKSTPDTGNENEGQCL 326
Db 281 NLCTLAETIQTILKDI TSDSENSFNEIQSL 313

Search completed: May 9, 2003, 17:08:25
Job time : 13.8429 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:05:23 ; Search time 16.3006 Seconds
(without alignments)
1846.092 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWTAVLPLVLGSQLRVH.....KDLGKSTPDGTGNEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1804	100.0	327	10	US-09-802-669-66
2	1166	64.6	204	10	US-09-948-018-18
3	863.5	47.9	669	9	US-10-226-296-3
4	863.5	47.9	669	9	US-10-226-318-3
5	856	47.5	335	10	US-09-826-212-7
6	856	47.5	335	10	US-09-802-669-2
7	856	47.5	335	10	US-09-949-713-20
8	856	47.5	335	10	US-09-874-138-4
9	856	47.5	335	10	US-09-884-987-2
10	856	47.5	335	10	US-09-935-727-9
11	856	47.5	335	12	US-10-005-842-4
12	844	46.8	335	9	US-09-314-889-6
13	844	46.8	335	10	US-09-333-966-6
14	645	35.8	281	9	US-09-756-854-3
15	645	35.8	281	9	US-10-041-574-3
16	523	29.0	167	9	US-10-112-793-22
17	523	29.0	237	9	US-09-925-299-960
18	523	29.0	237	10	US-09-925-299-960
19	496	27.5	157	10	US-09-949-713-15

20	494.5	27.4	144	10	US-09-949-713-21	Sequence 21, Appl
21	494.5	27.4	159	10	US-09-949-713-23	Sequence 23, Appl
22	494.5	27.4	376	10	US-09-949-713-22	Sequence 22, Appl
23	470	26.1	128	10	US-09-949-713-9	Sequence 9, Appl
24	470	26.1	143	10	US-09-949-713-10	Sequence 10, Appl
25	470	26.1	360	10	US-09-949-713-11	Sequence 11, Appl
26	462	25.6	119	9	US-10-112-793-15	Sequence 15, Appl
27	460	25.5	119	10	US-09-800-909-5	Sequence 5, Appl
28	460	25.5	119	10	US-09-884-987-3	Sequence 3, Appl
29	460	25.5	119	10	US-09-800-908-14	Sequence 14, Appl
30	215	11.9	418	9	US-09-992-964-14	Sequence 14, Appl
31	215	11.9	418	10	US-09-887-879-14	Sequence 2, Appl
32	215	11.9	468	9	US-10-226-296-2	Sequence 2, Appl
33	215	11.9	468	9	US-10-226-318-2	Sequence 2, Appl
34	215	11.9	468	12	US-10-039-785-1	Sequence 1, Appl
35	209	11.6	77	9	US-10-112-793-24	Sequence 24, Appl
36	205	11.4	148	10	US-09-855-266A-2	Sequence 2, Appl
37	205	11.4	176	10	US-09-855-266A-1	Sequence 1, Appl
38	205	11.4	283	10	US-09-924-231-2	Sequence 2, Appl
39	205	11.4	283	10	US-09-934-289A-13	Sequence 13, Appl
40	205	11.4	283	10	US-09-935-727-31	Sequence 31, Appl
41	205	11.4	283	12	US-10-020-787-2	Sequence 2, Appl
42	204	11.3	283	12	US-10-066-209-2	Sequence 2, Appl
43	202	11.2	77	9	US-09-992-964-17	Sequence 17, Appl
44	202	11.2	77	10	US-09-887-879-17	Sequence 17, Appl
45	202	11.2	272	10	US-09-782-980-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-802-669-66
; Sequence 66, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dead, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802.669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-669-66

Query Match 100.0%; Score 1804; DB 10; Length 327;
Best Local Similarity 100.0%; Pred. No. 8.6e-125;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLWTAVLPLVLGSQLRVHQTGNTSISLKLRRRVHETDKNCSGLYQGGPFCQPCQ	60
Db	1	MLWTAVLPLVLGSQLRVHQTGNTSISLKLRRRVHETDKNCSGLYQGGPFCQPCQ	60
Qy	61	PGKKVDECKMNGTPTCAPCTEGKEYMDKNHYADKRCRRLCDDEHGLEVTNCTLTON	120
Db	61	PGKKVDECKMNGTPTCAPCTEGKEYMDKNHYADKRCRRLCDDEHGLEVTNCTLTON	120
Qy	121	TKCKCKPFDYCDSPGCEHVCRCASCEHGTLEPCTATSTNTNCRKQSPRNLMLLTLLVLLI	180
Db	121	TKCKCKPFDYCDSPGCEHVCRCASCEHGTLEPCTATSTNTNCRKQSPRNLMLLTLLVLLI	180
Qy	181	PLVFYIKYRKRKCKWRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDWTIOEAKKF	240

Db 181 PLVFIYKRRKCKWRQDDPSRTSSRETIPMNASNLSKYIPRIADMTIQEAKKF 240
QY 241 ARENNIKEGIDEIMHDSIQDTAEQKVQLLWCYQSHGSKSDAYODLIGLKAECRRTL 300
Db 241 ARENNIKEGIDEIMHDSIQDTAEQKVQLLWCYQSHGSKSDAYODLIGLKAECRRTL 300
QY 301 KFDQMVQKDLGKSTPDGTGNEGQCLE 327
Db 301 KFDQMVQKDLGKSTPDGTGNEGQCLE 327

RESULT 2
US-09-948-018-18
; Sequence 18, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-948-018-18

Query Match 64.6%; Score 1166; DB 10; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWIWAVPLVLVLAGSOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYOGGPFCCOPQ 60
Db 1 MLWIWAVPLVLVLAGSOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYOGGPFCCOPQ 60

QY 61 PGKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120
Db 61 PGKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120

QY 121 TKCKKAPDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPRNRLWLLTILVLLI 180
Db 121 TKCKKAPDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPRNRLWLLTILVLLI 180

QY 181 PLVFIYKRRKCKWRQDDPS 204
Db 181 PLVFIYKRRKCKWRQDDPS 204

RESULT 3
US-10-226-296-3
; Sequence 3, Application US/10226296
; Publication No. US20030036168A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
; Receptor 4), Member of the TNF-Receptor
; Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/226,296
FILING DATE: 23-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-226-296-3

Query Match 47.9%; Score 863.5; DB 9; Length 669;
Best Local Similarity 49.2%; Pred. No. 1.5e-55;
Matches 164; Conservative 54; Mismatches 108; Indels 7; Gaps 2;

QY 1 MLWIWAVPLVLVLAGSOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYOGGPFCC 56
Db 336 MLGIWITLLPLVLTISVARLSKSYNAQVTDINSKGLERKTVTVTQNLGLHHDGQFCH 395

QY 57 QPCQPKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 396 KCPFGERRARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDDEHGLEVEINCT 455

QY 117 LTQNTKCKKPPDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPRNRLWLLTIL 176
Db 456 RTQNTKCRCKPFPFCNSTVCEHCDPCTCKEHIKECTLTSTNTCKEGRSRLGLCLL 515

QY 177 VLLIPLVFIYKRRKCKWRQDDP---ESRTSSRETIPMNASNLSKYIPRIADMT 233
Db 516 LLPILVIVKREVKQTKRRHRKENGSHESPTLNPETVAINLSVDLSKYITTIAGVMT 575

QY 234 IQEAKKFARENNIKEGIDEIMHDSIQDTAEQKVQLLWCYQSHGSKSDAYODLIGLKA 293
Db 576 LSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLGKKEAYDYLKDLKKA 635

QY 294 ECRRLDKFQDMVQKDLGKSTPDGTGNEGQCCL 326
Db 636 NLCTLAETQITILKIDITSSENSFNRIQSL 668

RESULT 4
US-10-226-318-3
; Sequence 3, Application US/10226318
; Publication No. US20030073187A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
; Receptor 4), Member of the TNF-Receptor

Matches	165;	Conservative	54;	Mismatches	107;	Indels	8;	Gaps	3;
Qy	1	MLWIWAVLPVLVLAG----	SOLRVHTQGTSNISSESLKLRRRRYHVEDTKNCSEGLYOGGFPCC	56					
Dd	1	MLGIWTLLPLVLTVARLSKSVAQAQYTDINSKLELRTVTVTETQNLEGHLHGDOGFCFCH	60						
Qy	57	QPCPGKKKVVEDCKMNGGTPTCAPCTEGEKYMDKNHYADKRCRCTLCDDEEHGLEVEYNCT	116						
Dd	61	KPCPPGERKARDCTVNGDEPDCVPCEQGEKEYTDRAHFSKRCRCRLCDEGHGLEVEINCT	120						
Qy	117	LTQNTKCKCPDFDYCDSPGCHEVCVRACSEHGTTLEPOTATSNTRCKOSPNRWLLTLIL	176						
Dd	121	RTQNTKRCKPNFFCNFTVCEBHDPCPKCEHGIIKECTLTNTKCKEGRSNLGWLCIL	180						
Qy	177	VLLIPL-VFIYRKVKRKKWKRRDDP---ESRTSSRETIPMNASNLSKYIPRIADM	232						
Dd	181	LPLPIVWVKRKEVQTCRKHKENGSGSHESPITNPETAISLDSDLYSKYITTIAGVM	240						
Qy	233	TIQAEKFARENNIKEGIDIEIMHDSIQDTAEQKVQLLWCYOSHGSKDAVDLIKGLKK	292						
Dd	241	TLISOQGFVRKNGVNEAKIDEIKNDVNQDIAEQKVQLLRNWHQLHGKKEAYDLTIKLKK	300						
Qy	293	AECRRTLDKQDMVQKDLGKSTPDPTGNENEGCOL	326						
Dd	301	ANJCTLAETKOTITILKDITSDSENSPRNIQS	334						

Query Match	47.5%	Score 856	DB 10	Length 335
Best Local Similarity	49.4%	pred. No. 2.5e-55		
Matches 165	Conservative 54	Mismatches 107	Indels 8	Gaps 3
QY	1	MLWIAVLPLVLAG----	SOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCC	56
Db		:	: : : : : : : :	
QY	1	MLGIWTLLPLVLT	SVARLSKSVNAQVTDINSKGLRLKVTVTVTQNLGLHHGQFCH	60
Db		:	: : : : : : : :	
QY	57	QPCOPGKKKYEDCKMNGGTPCTAPCTEGKFWMDKNHYADKRCRCTLDEBHGLEVEINCT	116	
Db		:	: : : : : : : :	
QY	61	KPCPPGGRKARDCTVNGDEDFPCQBGKGYTKRAHFSKRCRCLDEGHGLEVEINCT	120	
Db		:	: : : : : : : :	
QY	117	LTQNTKCKCKPDFCYDSPGCEHCVRACSCBHGTLPCPTATSNCRKQSPNRNLWLLTIL	176	
Db		: :	: : : : : : : :	
QY	121	RTQNTKCRCKPNFFCSTVCEHCDPCTCKEHIKECTLTSTNCKEGRSRNLGWJCLL	180	
Db		: :	: : : : : : : :	
QY	177	VLLIPL-VFIYRYRKRKKWKRRQDDP----	ESTSSRETIPMNASNLISKYIPRIAE	232
Db		: : : : : : : :	: : : : : : : :	
QY	181	LLPIPLIVVWYKRKEVQTKCRKRKENQGHSESTPLNPETVAINLSDVLSKYITTTIAGVM	240	
Db		: : : : : : : :	: : : : : : : :	
QY	233	TIOEAKKFARENNIKEGKIDEIMHDSITDPTAEQKVOLLICWYQSHGSKSDAYQDLIKGLKK	292	
Db		: : : : : : : :	: : : : : : : :	
QY	241	TLISOVGKGFVRKGVGNVNAKIDEIKNDVQDTAEQKVOLLRNWHLGKKEAYDTLILKDLKK	300	
Db		: : : : : : : :	: : : : : : : :	

```

QY 293 AECRTLDKFDWMQVKGSLGKSTPTDGTNENEGQCL 326
      : : : : : : : : : : : : : : : : : :
DB 301 ANLCTLAEKIQTILKDISDSENSFRNEIQSL 334

RESULT 8
US-09-874-138-4
; Sequence 4, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
;   APPLICANT: Ni, Jian
;   APPLICANT: Gentz, Reiner L.
;   APPLICANT: Yu, Guo-liang
;   APPLICANT: Rosen, Craig A.
;   TITLE OF INVENTION: Death Domain Containing Receptor 5
;   FILE REFERENCE: 1488.1310006
;   CURRENT APPLICATION NUMBER: US/09/874,138
;   CURRENT FILING DATE: 2001-06-06
;   PRIOR APPLICATION NUMBER: 09/565,009
;   PRIOR FILING DATE: 2000-05-04
;   PRIOR APPLICATION NUMBER: 60/148,939
;   PRIOR FILING DATE: 1999-08-13
;   PRIOR APPLICATION NUMBER: 60/133,238
;   PRIOR FILING DATE: 1999-05-07
;   PRIOR APPLICATION NUMBER: 60/132,498
;   PRIOR FILING DATE: 1999-05-04
;   PRIOR APPLICATION NUMBER: 09/042,583
;   PRIOR FILING DATE: 1998-03-17
;   PRIOR APPLICATION NUMBER: 60/054,021
;   PRIOR FILING DATE: 1997-07-29
;   PRIOR APPLICATION NUMBER: 60/040,846
;   PRIOR FILING DATE: 1997-03-17
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 4
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-874-138-4

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Query Match      47.5%; DB 10; Length 335;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY      1 MLWTAVLPLVLG---SOLRVITQGTNSTSESILKRRRVHETDKNCSEGLYOGGPPCC 56
      Db      1 MGIWTLLPLVLTSVARLSSKSVNAQVTDINSGLEGLKRTVTVETONLEGLHDGQFCH 60

QY      57 QPCPGKKKEDCKMNGGTPPCAPCTEGKEYMDKNHYADKRCRCTLGDEEHGLEVEVNC 116
      Db      61 KPCPPGKARKADCTVNGDEPDVCPQEGKEYTDKAHSSKCRRCRCLCDEGHGLEVEINCT 120

QY      117 LTQNTKCKCKPDFYCDSPGCEHCVRCA SCHEGLTEPCTATSNTRCKQSPNRNLWLLTIL 176
      Db      121 RTQNTKCRCPNFCNVTVCHECDPCTKCEGIIKECTLTSNTKCKEGSRNLGWLJCLL 180

QY      177 VLLIPL-VFYIRKYRKCKWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAE 232
      Db      181 LLPLPLVWKRKEVCTKRRKKNENGSHESPTLNPTVAIINLSDVDLSKYITTIAGVM 240

QY      233 TIQEAKKFARENNIKEGIDIEIMHDSIQDTAEQKVQLLCLWCYQSHGSKSDAYQDLIKGLKK 292
      Db      241 TLSQVKGFVRKNGVNEAKIDIEIKNDNVQDTAEQKVQLLRNWHQLHGCKEAYDTFLIRDLKK 300

QY      293 AECRRTLDKFQDMVKQDLGKSTPDTGNENEGCL 326
      Db      301 ANLCTLAERKIQTLILKDLTSDSENSFRNEIQSL 334

RESULT 9
US-09-884-987-2
: Sequence 2, Application US/09884987

```


APPLICATION NUMBER: US 60/040,846
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
TELEFAX: 3013098439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-005-842-4
Query Match 47.5%; Score 856; DB 12; Length 335;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIAVLPVLAG----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGPPCC 56
DB 1 MLGIWTLPLVLTSLVRLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCQPGKKVEDCKNGGTPTCAPCTEGKEKMDKNHYADKRCCTCLDDEHGLEVEINCT 116
DB 61 KPCPPGERKARDCTVNGDEPDVPCQEGKEKMDKNHYADKRCCTCLDDEHGLEVEINCT 120
QY 117 LTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 176
DB 121 RTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 180
QY 177 VLLIPL-VFIVRYKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLSKYIPRIADM 232
DB 181 LLPIPLVWVRKKEVQKTCRKRKENGSHESPTLNPTVAINLSVDLSKYITTIAGVM 240
QY 233 TIQEAKEFARENNIKGKIDIMHDSIQDTAEQVQLLWYQSHGSKSDAYQDLIKGLK 292
DB 241 TLSQVKGFEVRKNGVNEAKIDEIKNDVQDTAEQVQLLRNWHQHLGKKEAYDTLIKDLK 300
QY 293 AECRRRLDKFQDMVQKDLGKSTPDTGNEGQCL 326
DB 301 ANCLTAEKIQITILKIDITSSENSFRNEIQSL 334

RESULT 12
US-09-314-889-6
Sequence 6, Application US/09314889
Publication No. US20030077694A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/314,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/815,469
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-314-889-6

Query Match 46.8%; Score 844; DB 9; Length 335;
Best Local Similarity 49.1%; Pred. No. 1.9e-54;
Matches 164; Conservative 54; Mismatches 108; Indels 8; Gaps 3;

QY 1 MLWIAVLPVLAG----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGPPCC 56
DB 1 MLGIWTLPLVLTSLVRLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCQPGKKVEDCKNGGTPTCAPCTEGKEKMDKNHYADKRCCTCLDDEHGLEVEINCT 116
DB 61 KPCPPGERKARDCTVNGDEPDVPCQEGKEKMDKNHYADKRCCTCLDDEHGLEVEINCT 120
QY 117 LTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 176
DB 121 RTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 180
QY 177 VLLIPL-VFIVRYKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLSKYIPRIADM 232
DB 181 LLPIPLVWVRKKEVQKTCRKRKENGSHESPTLNPTVAINLSVDLSKYITTIAGVM 240
QY 233 TIQEAKEFARENNIKGKIDIMHDSIQDTAEQVQLLWYQSHGSKSDAYQDLIKGLK 292
DB 241 TLSQVKGFEVRKNGVNEAKIDEIKNDVQDTAEQVQLLRNWHQHLGKKEAYDTLIKDLK 300
QY 293 AECRRRLDKFQDMVQKDLGKSTPDTGNEGQCL 326
DB 301 ANCLTAEKIQITILKIDITSSENSFRNEIQSL 334

RESULT 13
US-09-333-966-6
Sequence 6, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington

APPLICANT: NI, Jian
 Yu, Guo-Liang
 Fan, Ping
 Gentz, Reiner
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TF9
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/756,854
 FILING DATE: 10-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/095,094
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Kenley K.
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PF375
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 PS-09-756-854-3

[illegible]

RESULT 15
US-10-041-574-3
; Sequence 3, Application US/10041574
; Patent No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian

; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Fan, Ping
 ; APPLICANT: Gentz, Reiner L.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 ; FILE REFERENCE: PF375P1
 ; CURRENT APPLICATION NUMBER: US/10/041,574
 ; PRIOR FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: 09/527,236
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/052,991
 ; PRIOR FILING DATE: 1997-06-11
 ; PRIOR APPLICATION NUMBER: 09/095,094
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/126,019
 ; PRIOR FILING DATE: 1999-03-24
 ; PRIOR APPLICATION NUMBER: 60/134,220
 ; PRIOR FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-041-574-3

Query Match 35.8%; Score 645; DB 9; Length 281;
 Best Local Similarity 45.6%; Pred. No. 5.8e-40;
 Matches 128; Conservative 46; Mismatches 97; Indels 10; Gaps 4;

Qy	1	MLTIWVLPVLAG----	SQLRVHTQGTNSISELKLRRRVHETDKNCSEGLYOGGPCC	56
Db	1	MLGIWTLPLVLT	SVARLSSKSVNAQYTDINSKGLERKVTVTETONLEGLHHDGQFCH	60
Qy	57	OPCOPGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYNCT	116	
Db	61	KPCPPGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRCRLCDEGHGLEVEINCT	120	
Qy	117	LTQNTKCKPDPFYCDSPGCEHCVCASCCEHGTLEPCTATSNINCRKQSPNRNLWLTIL	176	
Db	121	RTQNTKCRKPFNFCNSTVCEHCDPCTKCEHIIKECTLTSTNCKKEGSRNLGLCLL	180	
Qy	177	VLLIPL-VFYRYKRYKRCWKRRQDDP--ESRTSSRETIPMNASNLSLSKYIPRIAEQM	232	
Db	181	LLPIPLIVWVKRKEVOKTCRKRKENOGSHESPTLNPETVAINLSVDVLSKYITTTIAGVM	240	
Qy	233	TIOEAKK--FARENNIKEGIDEIMHDSIODTAEOKVQLLL	271	
Db	241	TLQVKANLCTLAEKIQTIIILKDITSDSENSFRNEIQSLV	281	

Search completed: May 9, 2003, 17:09:17
 Job time : 26.3006 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 17:02:31 ; Search time 28.1556 seconds
(without alignments)
1116.509 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWIWAVLPLVLGSQLRVH.....KDLGKSTPTDGNENEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	327	A46484	apoptosis-mediati
2	1058.5	58.7	324	JC2395	Fas antigen precu
3	856	47.5	335	A40036	apoptosis-mediati
4	810.5	44.9	314	I37383	FAS soluble protei
5	305.5	16.9	149	S58662	Fas-Delta-(4,7) pr
6	203.5	11.3	271	S12783	Ox40 antigen precu
7	202	11.2	272	I48700	gene ox40 protein
8	194.5	10.8	277	A60771	B-cell activation
9	189.5	10.5	455	1 GQWU71	tumor necrosis fac
10	185	10.3	454	1 GQWU71	tumor necrosis fac
11	183	10.1	260	A46517	CD27 antigen precu
12	179.5	10.0	435	1 I54182	tumor necrosis fac
13	179	9.9	461	1 GQRTT1	tumor necrosis fac
14	171	9.5	277	1 I37552	Ox40 homolog - hum
15	169	9.4	461	1 JC4302	tumor necrosis fac
16	167	9.3	250	1 A49053	CD27 antigen precu
17	165.5	9.2	416	1 JN0006	nerve growth facto
18	165	9.1	305	2 A46476	B cell-associated
19	165	9.1	349	2 D72175	G2R protein - vari
20	163	9.0	348	2 T28623	hypothetical prote
21	163	9.0	349	2 D36858	gene G4R protein -
22	154.5	8.6	425	1 A26431	nerve growth facto
23	154.5	8.6	595	1 A42086	CD30 antigen precu
24	148	8.2	461	1 A35356	tumor necrosis fac
25	141	7.8	427	1 GQWU71	nerve growth facto
26	135.5	7.5	677	2 C42125	trophozoite cystei
27	126.5	7.0	1372	2 T25933	hypothetical prote
28	126	7.0	493	2 JC5486	membrane glycoprot
29	123.5	6.8	459	2 I48854	gene murine tumour

ALIGNMENTS

RESULT 1

A46484

apoptosis-mediating membrane-associated polypeptide Fas - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A46484; A47254

R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenk

J. Immunol. 148, 1274-1279, 1992

A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas

A;Reference number: A46484; MUID:92148151; PMID:1371136

A;Accession: A46484

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-327 <WAT>

A;Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226

A;Experimental source: BAM3 macrophage cell line

A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)

R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993

A;Title: Aberrant transcription caused by the insertion of an early transposable ele

A;Reference number: A47254; MUID:93189576; PMID:7680478

A;Accession: A47254

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-96 <ADA>

A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506

A;Experimental source: MRL lpr/lpr

A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126

Ox40 antigen precu

C;Superfamily: NGF receptor repeat homology

C;Keywords: transmembrane protein

F;44-79/Domain: NGF receptor repeat homology <NGF>

F;81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 100.0%; Score 1804; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 6.9e-122;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLWIWAVLPLVLGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPCCPCQ	60
Db	1	MLWIWAVLPLVLGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPCCPCQ	60
Qy	61	PGKKVDECKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN	120
Db	61	PGKKVDECKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN	120
Qy	121	TKCKCKPDFYCDSPGCEHCVCASCCEHGTLEPCTATSNTRKOSPRNRLMLLTLVLLI	180
Db	121	TKCKCKPDFYCDSPGCEHCVCASCCEHGTLEPCTATSNTRKOSPRNRLMLLTLVLLI	180
Qy	181	PLVFIYKRYKRRKCKWKRQDDPESRTSSRTIPMNASNLSSKYPITRAEDMTTQEA	240
Db	181	PLVFIYKRYKRRKCKWKRQDDPESRTSSRTIPMNASNLSSKYPITRAEDMTTQEA	240

QY 241 ARENNKEGKIDEIMHDSIQDTAEQKVQLLWCYQSHGSKSDAYODLIGLKKAECCRTLD 300
|||||
Db 241 ARENNKEGKIDEIMHDSIQDTAEQKVQLLWCYQSHGSKSDAYODLIGLKKAECCRTLD 300
|||||
QY 301 KFDQVMQKDLGKSTPDGTGNEGQCILE 327
|||||
Db 301 KFDQVMQKDLGKSTPDGTGNEGQCILE 327
|||||
RESULT 2
JC2395
Fas antigen precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: JC2395; PC2246
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A:Reference number: JC2395; MUID:94128114; PMID:7507668
A:Accession: JC2395
A:Molecule type: mRNA
A:Residues: 1-324 <KIM>
A:Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468487
A:Experimental source: thymus
A:Accession: PC2246
A:Molecule type: mRNA
A:Residues: 1-62, 'RFT' <K12>
A:Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A:Experimental source: liver
C:Genetics:
A:Insertions: 62/1
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-324/Product: Fas antigen #status predicted <WAT>
F:44-79/Domain: NGF receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NGF>
F:171-188/Domain: transmembrane #status predicted <TMW>
Query Match 58.7%; Score 1058.5; DB 2; Length 324;
Best Local Similarity 61.1%; Pred. No. 1.5e-68;
Matches 201; Conservative 41; Mismatches 80; Indels 7; Gaps 3;
QY 1 MLWIAVPLVLVLAGSQLRVHTQCTNSISLKLRRRVHETDKNCSEGLYQGGPFCQPCQ '60
|||||
Db 1 MLWIAVPLVLVLAGPELVNRMQGTDSIFEGLELKRVSRETDNCSSEGLYQVGPFCQPCQ 60
|||||
QY 61 PGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEFETNCTQN 120
|||||
Db 61 PGBRKVDCTTSGAPTCHECTEGEYTDKHYSDKRCRCAFCDEHGLEVEFETNCTRTQN 120
|||||
QY 121 TKCKKPFDPYCDSPGCEHCVRCASCE-HGTLEPCTATSNTRKQSPRRN-LWLLILVL 178
|||||
Db 121 TKCRKENYCNASLDCHGYCHTSCGLEDPCTRTSNCKKQSSNKLWLLILPGL 180
|||||
QY 179 LPLVPIVYKRYKRCWKRRQDDPESRTSPRETIPMNASNLISKYIPRIAEADMTIQEAK 238
|||||
Db 181 AILFVPIYKRYR-----KRQPDGSGIPSPESVPMNVSDVNLNKYIWRTEAKMKICDAK 235
|||||
QY 239 KFARENNEKGEKIDEIMHDSIQDTAEQKVQLLWCYQSHGSKSDAYODLIGLKKAECCRT 298
|||||
Db 236 KEARQHKIPESKIDEHNSPDAAEQKIQLLQWCYQSHGKTGACQALLQGLRKANRCDDI 295
|||||
QY 299 LKFDQVMQKDLGKSTPDGTGNEGQCILE 327
|||||
Db 296 AEEIQAMWEDHENSISNRNENEGOSLE 324
|||||
RESULT 3
A40036
apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1

C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C:Accession: A40036; S24543; A38142
R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.;
Cell 66, 233-243, 1991
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can
A:Reference number: A40036; MUID:91309137; PMID:1713127
A:Accession: A40036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <ITO>
A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
R:Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A:Reference number: S24543
A:Accession: S24543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <KRA>
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.;
J. Biol. Chem. 267, 10709-10715, 1992
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a mem-
A:Reference number: A38142; MUID:92268122; PMID:1375228
A:Accession: A38142
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-134, 'Q', 136-335 <OEH>
A:Experimental source: SKW6.4 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)
A:Note: in NCBI backbone the source is designated as mouse
C:Genetics:
A:Gene: GDB:APT1
A:Cross-references: GDB:132671; OMIM:134637
A:Map position: 10q24.1-10q24.1
C:Superfamily: NGF receptor repeat homology
C:Keywords: apoptosis; surface antigen; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:85-128/Domain: NGF receptor repeat homology <NG4>
F:174-190/Domain: transmembrane #status predicted <TMW>
Query Match 47.5%; Score 856; DB 2; Length 335;
Best Local Similarity 49.4%; Pred. No. 4.8e-54;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLWIAVPLVLVLAG-----SOLRVHTQCTNSISLKLRRRVHETDKNCSEGLYQGGPFCQ 56
|||||
Db 1 MLGIIWTLPLVLTAVARLSKSVNAQVTDINSKGLRLKRTVTIVETQNLGLHHDGQFCH 60
|||||
QY 57 QPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEFETNCT 116
|||||
Db 61 KPCPPGERKARDCTVNGDEPDPCVQCGEGEYTDKAHFSKRCRCLCDDEHGLEVEINCT 120
|||||
QY 117 LTQNTKCKKPFDPYCDSPGCEHCVRCASCEHGTLEPCTATSNTRKQSPRRNRLWLLTIL 176
|||||
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHLIKECTLSNTKCKEESRNLGLCLL 180
|||||
QY 177 VLLIPI-VPIYKRYKRCWKRRQDDP-----ESRTSSRETIPMNASNLISKYIPRIAEAD 232
|||||
Db 181 LPLIPLIVVWKRKEVQKTCRKHKENQSGHESPTLPETVAIINLSDVLSKYITTAGVM 240
|||||
QY 233 TTQEAKKFARENNKEGKIDEIMHDSIQDTAEQKVQLLWCYQSHGSKSDAYODLIGLKK 292
|||||
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHGKKEAYDTLIKDLKK 300
|||||
QY 293 AECRRTLDFQDMQVQKDLGKSTPDGTGNEGQCIL 326
|||||
Db 301 ANLCTLAEKIQIILKIDTSSENSENFNEIOSL 334
|||||
RESULT 4
I37383
FAS soluble protein - human

C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I37383
R: Cascino, I.; Flucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are
A:Reference number: I37383; MUID:95181785; PMID:7533181
A:Accession: I37383
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <RES>
A:Cross-references: EMBL:247993; NID:9728578; PIDN:CAA88031.1; PID:9695539

Query Match 44.9%; Score 810.5; DB 2; Length 314;
Best Local Similarity 46.8%; Pred. No. 8.1e-51;
Matches 156; Conservative 50; Mismatches 100; Indels 27; Gaps 3;

Qy 1 MLWNAVLPLVLG-----SQLRVHTQGTNSISLKLRRRVHETDKNCSGLYGGPPCC 56
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTTVETQNLEGLHHDGQFCH 60
Qy 57 QPCPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCT 116
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAAHFSSKCRCLDEGHVNNESSRN 120
Qy 117 LTQNTKCKPDPFYCDSPGCEHCVRASCERTGTEPCTATNTNCRKSPRNRLMLLTL 176
Db 121 RTQNTKCKPDPFYCDSPGCEHCVRASCERTGTEPCTATNTNCRKSPRNRLMLLTL 176
Qy 177 VLLPLFIYKRYKRCWKRRQDDP---ESRTSSRETIPNANSLSLKPIPIAEDMT 233
Db 169 -----VKRKEYQKTRKHENQGSHPSTLNPETVAINLSVDLSKYITTIAGVMT 220
Qy 234 IOEAKPARENKKEGKIDETMHDSDIOPTAEQVQLLCWYQSHGSKSDAYQDLKGLAKA 293
Db 221 LSQVKGFRKNGVNEAKIDEKNDVQDTAEQVQLLRNWHQLHGKRAYDTLINDLAKA 280
Qy 294 ECRTLDKFDQMDKDGKSTPDPTGNEGQCL 326
Db 281 NLCTLAERKIOTIILKDTSDSENSFRNEIQSL 313

RESULT 5

S58662
Fas-Delta-(4,7) protein - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 01-Dec-2000
C:Accession: S58662; S57566
R: Liu, C.; Cheng, J.; Mountz, J.D.
Biochem. J. 310, 957-963, 1995
A:Title: Differential expression of human Fas mRNA species upon peripheral blood mononuc
A:Reference number: S58662; MUID:96013198; PMID:7575433
A:Accession: S58662
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-149 <LIU>
R: Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57565
A:Accession: S57566
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <SCH>
C:Cross-references: EMBL:X89101; NID:9887457; PID:9887458
C:Keywords: alternative splicing

Query Match 16.9%; Score 305.5; DB 2; Length 149;
Best Local Similarity 42.9%; Pred. No. 5.5e-15;
Matches 63; Conservative 20; Mismatches 47; Indels 17; Gaps 4;

Qy 1 MLWNAVLPLVLG-----SQLRVHTQGTNSISLKLRRRVHETDKNCSGLYGGPPCC 56
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTTVETQNLEGLHHDGQFCH 60

Qy 57 QPCPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVET--- 113
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAAHFSSKCRCLDEGHVNNESSRN 120
Qy 114 -NCTLTQNTKCKPDP-----FYC 131
Db 121 AHSPTAPSAKRK-DPDLTWGGFVFPFC 146

RESULT 6

SI2783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: SI2783; S08036
R: Mallett, S.; FCSsum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lympho
A:Reference number: SI2783; MUID:90214614; PMID:2157591
A:Accession: SI2783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C:Superfamily: CD27 antigen; NGF receptor repeat homolog
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-27/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 11.3%; Score 203.5; DB 2; Length 271;
Best Local Similarity 24.4%; Pred. No. 1.9e-07;
Matches 64; Conservative 27; Mismatches 82; Indels 89; Gaps 11;

Qy 2 LWINAVLP--LVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSGLYGGPPCCQPC 59
Db 1 MYVWVQQPTAFLLGLSLGV-----TVKL-----NCVKDTYPSGHKCCRC 41
Qy 60 QPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTO 119
Db 42 QPHGMSRCDHTRDT-VCHPCEPG-FYNEAVNY-DTCQCTQCHRSGLKQNCPTPE 98
Qy 120 NTKCKKPDFY-----CD-----SPG-----CEHCVRASCERTGTEPCTAT 156
Db 99 DTVCQCEPGTQPRODSSHKLGVDCVPCPPGHPSPGNSQACKPWTNCTLSGKQIRHPASNS 158
Qy 157 SNTNCRKOS-----PRNRLMLTI----- 175
Db 159 LDTVCEDRSLLATLLWETQRTTFRPTTVPSTTVPRTSQLPSTPTLVAPEGPAFVILGL 218
Qy 176 -LVLLIPLVFIYKRYKRCWK 196
Db 219 GLGLIAPLTVLLALYLLRKMR 240

RESULT 7

I48700
gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R: Calderhead, D.N.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A:Reference number: I48700; MUID:94044750; PMID:8228223
A:Accession: I48700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CAA79772.1; PID:9312828
R: Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.

Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A:Reference number: I48334; MUID:95255413; PMID:773295
A:Accession: I48334
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14,'G',16-272 <RE>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: OX40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 11.2%; Score 202; DB 2; Length 272;
Best Local Similarity 26.5%; Pred. No. 2.5e-07;
Matches 69; Conservative 22; Mismatches 85; Indels 84; Gaps 12;

OY 2 LWIWAFLVLAGSOLRVHTGTNISLSKLRVHETDKNCSEGLYGGPFCCQPCQP 61
DB 1 MIVWVQQPTALL---LLALTILGVTA-----RRRL---NCVKHTYPSGHKCCRECQP 44
OY 62 GKKKVEDCKMNGGPTCAPCTEGKEYMDKNHYADKRCCTLCDEHGLEVTNCTLTONT 121
DB 45 GHGWSVRCDHRTDT-LCHPCETG-FYNEAVNY-DTCQCTQCNHRSSELKQNCPTQDT 101
OY 122 KCKKPDY-----CD-----SPG-----CEHCVC----- 142
DB 102 VCRCPGTQPRQDSYKLGVDVCPGPFHFGNNGACKPWNTLSGKQTRHPASDLD 161
OY 143 ASCE-----HGILEPCTATNTNCRKQS-----PNRLWLLTIL 176
DB 162 AVCEDSLATLWETORPTFRPTVQSTVWPTSELSPPTLVTPGPAFALLGLGL 221
OY 177 VLLIPLVFIYKRYKRCWK 196
DB 222 GLLAPLTVLLALYLLRAWR 241

RESULT 8
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
A:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608; PMID:2475341
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A:Reference number: A60771; MUID:89093941; PMID:2463309
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:2194-2195/Domain: extracellular #status predicted <EXT>
F:194-2195/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.8%; Score 194.5; DB 2; Length 277;
Best Local Similarity 28.6%; Pred. No. 8.6e-07;
Matches 59; Conservative 20; Mismatches 74; Indels 53; Gaps 8;

OY 37 VH-ETDKNCSEGLYGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYAD 95
DB 18 VHPPTACREKQYLINSQCCLQPGKLVSDCTFTET-ECLPCGE-SEFLDTWNRRT 75
OY 96 KCRCTLCDEHGLEVTNCTLTQNTKCKPDKDFYCDSPGCHVCRCASCEHG----- 148
DB 76 HCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACSCVLHRSCLSPGFGVKQIA 135
OY 149 -----TLEPCTA--TSN-----TNCRKO-----SPRNLWLL 173
DB 136 TGVSDTICEPCVPGFVSNSAFKCHPWTSCETKDLVVQAGTNKTDVVCGPQDRLRAL 195
OY 174 TIL-----VLLIPLVFIYKRYK 191
DB 196 VVIPIIFILFAILLVLVFIKRVK 221

RESULT 9
GQUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
A:Accession: A38208; A34899; A36555; C36555; A38281; S12057; JT0758; A60231;
R:Fuchs, P.; Struhl, S.; Dworzak, M.; Hummler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p50) gene (TNRF1) and localization t
A:Reference number: A38208; MUID:92250049; PMID:131517
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; P
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Les
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor r
A:Reference number: A34899; MUID:90235284; PMID:2158862
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A:Experimental source: placenta
A:Note: part of this sequence, including the amino end of the mature protein, confir
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fac
A:Reference number: A34900; MUID:90235285; PMID:2158863
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R:Hummel, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, P
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK',98-100-104;107-128;162-167,'X',16
A:Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R:Gray, P.W.; Barrett, K.; Chantray, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A:Reference number: A38281; MUID:91017509; PMID:2170974
A:Accession: A38281

A:Molecule type: mRNA
A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
A>Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R:Nophr, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A>Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
le form of the receptor.
A:Reference number: S12057; MUID:91006021; PMID:1698610
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <KEM>
A:Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A>Note: Parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A>Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A:Reference number: JT0758; MUID:94085779; PMID:8262379
A:Accession: JT0758
A:Molecule type: DNA
A:Residues: 1-113 <KEM>
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A>Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A>Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A:Reference number: A38258; MUID:91062364; PMID:2174164
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyseil, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A>Title: Isolation and characterization of a tumor necrosis factor binding protein from
A:Reference number: A60594; MUID:89171156; PMID:2924890
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'Y', 55-57, 'XK', 60 <OLS>
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A>Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A>Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: JC2404; MUID:95128033; PMID:7765720
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFRI
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status

F:44-82/Domain: NGF receptor repeat homology <NGL>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane status predicted <MEM>
F:235-455/Domain: intracellular status predicted <INT>
F:54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted
Best Match 10.5%; Score 189.5; DB 1; Length 455;
Best Local Similarity 24.7%; Pred. No. 3.le-06;
Matches 67; Conservative 31; Mismatches 112; Indels 61; Gaps 11;
QY 7 VLPLVLAGSOLRVHTQGTNISSESLKLRVRVHETDKNCSEGLY---OGGPFCCOPCPQPGK 63
Db 10 LLPLVLELLVGVIPSGVIGLVPHLPDREK---RDSVCPQPKYIHPQNNSTCCCTCKHGT 66
QY 64 KKVEDCKKNGTPTCAPCTGEGKEYMDKNHVDKCRRTCLDEBHGLEVETNCTLTONTKC 123
Db 67 LYNDGPGQDPTDCECSGSFTASENHLR-HCLSGSKRKGEMQVEISSCTVDRTVC 125
QY 124 KCRPDFYCD--SPGCEHCVRCAECHEGTLT-PCTATSTNT-----NC 161
Db 126 GCRKNQVRHYWSENLFCQFNCGLNGTVHLSQCEKQNTVCTCHAGFFLRENECVCSNC 185
QY 162 RKQSPRNLWL-----LTIL-----VLLPLVFIYKRYKRCWK---- 196
Db 186 KKSLECKKLCPLQETENYKGTEDSGTTLPLVIFVFGLLSLFLGLMYRQYR-WKSKLY 244
QY 197 -----RRQDDPESRTSSRETIPMNASLSLS 222
Db 245 SIVCGKSTPEKEGELEGTGTTKPL-APNPSFS 274
RESULT 10
QOMST1
tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence.revision 30-Jun-1992 #text.change 01-Dec-2000
C:Accession: A38634; B40254; S16677; S19021; I34532; I57826
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A>Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis fact
A:Reference number: A38634; MUID:91187885; PMID:1849278
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.;
Mol. Cell. Biol. 11, 3020-3026, 1991
A>Title: Molecular cloning and expression of the type 1 and type 2 murine receptors
A:Reference number: A40254; MUID:91246168; PMID:1645445
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <GO2>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fe
Eur. J. Immunol. 21, 1649-1656, 1991
A>Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necr
A:Reference number: S16677; MUID:91285014; PMID:1647956
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R:Rothe, J.G.; Brückhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A>Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A:Reference number: S19021; MUID:92039815; PMID:1657766
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Bebo, B.F.

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Db 238 ITEVKEFYKNGWEAKIDIDIMHDLHETAQKVOLLRWYQSHGKNAYCTLTNLPRK 297
QY 294 ECRRTLDKFDQVMDKLGKSTPDTGNENEGQCL 326
Db 298 ----LAEXICDVLKIDITNERENANLQNESEN 326

RESULT 11
Q9GK28 ID Q9GK28 PRELIMINARY; PRT; 310 AA.
AC Q9GK28;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fas antigen APO-1/CD95.
GN FAS.
OS Macaca arctoides (Stump-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9540;
RN [1]
RP SEQUENCE FROM N.A.
RA Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;
RT "Cloning of fas gene in stump-tailed monkey.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332357; AAC49394.1; -
DR HSSP; P25445; IODF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 310 AA; 34806 MW; C5C79BF1F804A419 CRC64;

Query Match 42.6%; Score 768; DB 6; Length 310;
Best Local Similarity 47.6%; Pred. No. 3.2e-60;
Matches 156; Conservative 41; Mismatches 101; Indels 30; Gaps 6;

QY 1 MLWIAVPLVPLVLSQLR-----VHTQGISISSESLKRRVHETDKNCSEGLYQGGPFC 55
Db 1 MLCWTLLPLVLT-SVRLLSKCVNAQVTDISSKGFELRKIVTTIETQNLGLHHEGQFC 59
QY 56 CQCPQKXKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVEYTC 115
Db 60 RNPCCPGERKARDCTVNEDEPDCVPCQEGKEYTDKGFSSKRCRCRLCDEGHGLEVEINC 119
QY 116 TLQNTKCKGKPDFYCDSPGCEHVCASCSEHGTLPCTATSNTRKQSPRNLWLLTI 175
Db 120 TRQNTKCKGKPDFYCDSPGCEHVCASCSEHGTLPCTATSNTRKQSPRNLWLLTI 175
QY 176 LVLLIPLVFIYKRYKRCWKRRQDDPESRTSSRETIPNANSLSKYIPRIADMTIQ 235
Db 169 -----VVKPCRKHR--KENQGPHESTLNPET-AINLSDVDLSKYITTIAGAMTILS 218
QY 236 EAKKFARENNIKGIDEIMHDSIQDTAQKVOLLWCYQSHGKSDAYODLLKGLKKAC 295
Db 219 QVKDFVRKNGVSEAKIDEIKNNHVQDTAQKVOLLRWYQSHGKSDAYODLLKGLKKAC 295
QY 296 RTLDKFDQVMDKLGKSTPDTGNENEG 323
Db 279 CTLAEKIHAVILKDI---TSDTENSNGF 303

RESULT 12
Q9R230 ID Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;

Db 238 ITEVKEFYKNGWEAKIDIDIMHDLHETAQKVOLLRWYQSHGKNAYCTLTNLPRK 297
QY 294 ECRRTLDKFDQVMDKLGKSTPDTGNENEGQCL 326
Db 298 ----LAEXICDVLKIDITNERENANLQNESEN 326

RESULT 13
Q9XS60 ID Q9XS60 PRELIMINARY; PRT; 263 AA.
AC Q9XS60;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fas antigen spliced variant.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021297; BAA78429.1; -
DR HSSP; O14763; IDAV.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 263 AA; 30374 MW; 6D76782ADEDBFD7 CRC64;

Query Match 28.9%; Score 520.5; DB 6; Length 263;
Best Local Similarity 48.8%; Pred. No. 2.6e-38;
Matches 100; Conservative 27; Mismatches 61; Indels 17; Gaps 4;

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SQ SEQUENCE 334 AA; 37531 MW; 2DC5B1661C13191C6 CRC64;
Query Match 45.2%; Score 815; DB 6; Length 334;
Best Local Similarity 49.4%; Pred. No. 2.3e-64;
Matches 164; Conservative 46; Mismatches 108; Indels 14; Gaps 6;

QY 1 MLWTWAVLPLVLAGSQL-----VHTQGTNSISESLKRRRVHETDKNCSEGLYQGPGFC 55
DB 1 MLGFWTLPLVLT-SVVRLLSKVIAQVTDISSKGFLRKIVTTIETQNLGLHHEGQFC 59

QY 56 CQCPQCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINC 115
DB 60 RNPCCPPGERKARDCTVNEDEPCVQCEGKEYTDKGHLSSKRRRCRLCDDEHGLEVEINC 119

QY 116 TLQNTKCKKPFYCDSPGCEHCVRCASEHGHTLEPCTATNTNCRKQSPNRNL-WLLT 174
DB 120 TRTQNTKCKKPNFNCNSAVCEHCDPRICKKHGIEECTLTNTKKEEDSRDLPLWCL 179

QY 175 ILVLLIPLVFIYKRYKRCWKRRQDPPESRTSSRETIPMNASNLSSKYIPRIADMTI 234
DB 180 LLLLPIPIVVVYKACRKHRENQGPHESTTLNPET-AINLSDVLSKYITTIAGMTL 238

QY 235 QEAKKFARENNITKEGKIDIMHDSIQDTAEQVOLLWCYQSHGKSDAYQDLIKGLKAE 294
DB 239 SOVKDFVRKNGVSEAKIDEIKNDVQDTAEQVOLLWRNYQHLGKDKACDTLLIKGLKAD 298

QY 295 CRTLDKFDQMVQKDLGKSTPDTGNEG 323
DB 299 LCTLAEKIHAIVILKDI---TSDTENSNG 324

RESULT 10
O97491 PRELIMINARY; PRT; 327 AA.
ID O97491 AC O97491; (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Fas protein.
GN FAS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIMPHOCYTE;
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT "Cloning of sheep fas antigen."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011671; BAA37093.1;
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;

Query Match 44.5%; Score 802; DB 6; Length 327;
Best Local Similarity 47.7%; Pred. No. 3.2e-63;
Matches 159; Conservative 48; Mismatches 112; Indels 14; Gaps 5;

QY 1 MLWTWAVLPLVLAGSQL-----RVHTQGTNSISESLKRRRVHETDKNCSEGLYQGPGFC 54
DB 1 MSGIWHLSLIFISVSRPLSKGENAHVAGIN--SEGLFLNKNITGA--SSCOEGLYRHLF 57

QY 55 CCQCPQCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEIN 114
DB 58 CCQCPQCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEIN 117

QY 115 CTLQNTKCKKPFYCDSPGCEHCVRCASEHGHTLEPCTATNTNCR-KQSPNRNLWLL 173
DB 118 CTRQNTKCKKPNFNCNSAVCEHCDPRICKKHGIEECTLTNTKKEEDSRDLPLWCL 177

QY 174 TLVLLIPLVFIYKRYKRCWKRRQDPPESRTSSRETIPMNASNLSSKYIPRIADMTI 233
DB 178 LTLVLLIPLVFIYKRYKRCWKRRQDPPESRTSSRETIPMNASNLSSKYIPRIADMTI 237

QY 234 IQEAKKFARENNITKEGKIDIMHDSIQDTAEQVOLLWCYQSHGKSDAYQDLIKGLKKA 293
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RESULT 4
Q9BDN0
ID Q9BDN0 PRELIMINARY; PRT; 331 AA.
AC Q9BDN0
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE FAS antigen CD95.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21383618; PubMed=11491535;
RX Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344850; AAK37610.1; -
DR HSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00020; TNFR_C6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR VARIANT 75 75 V->A.
FT VARIANT 89 89 E->K.
FT VARIANT 196 196 E->K.
FT VARIANT 201 201 R->H.
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 45.8%; Score 825.5; DB 6; Length 331;
Best Local Similarity 49.8%; Pred. No. 2.7e-65;
Matches 164; Conservative 46; Mismatches 108; Indels 11; Gaps 5;

QY 1 MLWTAVLPVLVAGSOLR-----VHTQGTNSISLSKLRRRVHETDKNCSEGLYOGGPF 55
DB 1 MLGIWTLPLVLT-YVRLLSKCVNAQVTDISSKGFELRKIVTTIETQNLGLHHGQFC 59
QY 56 CQCPQKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTCTCDEHGLEVEYNC 115
DB 60 RNPCCGERKARDCTVNEDEPDCVPCQEGEYTDKGHFSSKRCRLCDEHGLEVEINC 119
QY 116 TLQNTCKCKPDPYCDSPGCEHCVCASCHEGTLEPCTATSNTRCKQSPRNL-WLLT 174
DB 120 TRQNTCKRCNPFNCFCNSAVCEHCDPCTCKKHGIEECTLTSTNPKCKEEDSRDLPLWCL 179
QY 175 ILVLLIPLVFIYRKRYKRCWKRRQDDPSRTSSRETIPMNASLSKYIPRIADMTI 234
DB 180 LLLLPVIVVVIKACKRKHKENQGPHESTYLNPEI-AINLSDVLSKYITTIAGMTL 238
QY 235 QEAKKFARENKIEGKIDIMHSDIQTAEQVOLLWCYQSHGKSDAYQDLIKGLKAE 294
DB 239 SQVKDFVRKNGVSEAKIDEIKNDVQDTAEQVOLLRNWYQLHGCKDCACTLIKGLTAD 298
QY 295 CRTLDKFDQVQKLGKSTPDGTGNEG 323
DB 299 LCTLAEKIHAVILKDI---TSDTENSNGF 324

RESULT 5
Q9BDP2
ID Q9BDP2 PRELIMINARY; PRT; 333 AA.
AC Q9BDP2
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE FAS antigen CD95.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21383618; PubMed=11491535;
RX Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344850; AAK37610.1; -
DR HSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00020; TNFR_C6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 45.8%; Score 825.5; DB 6; Length 331;
Best Local Similarity 49.8%; Pred. No. 2.7e-65;
Matches 164; Conservative 46; Mismatches 108; Indels 11; Gaps 5;

QY 1 MLWTAVLPVLVAGSOLR-----VHTQGTNSISLSKLRRRVHETDKNCSEGLYOGGPF 55
DB 1 MLGIWTLPLVLT-YVRLLSKCVNAQVTDISSKGFELRKIVTTIETQNLGLHHGQFC 59
QY 56 CQCPQKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTCTCDEHGLEVEYNC 115
DB 60 RNPCCGERKARDCTVNEDEPDCVPCQEGEYTDKGHFSSKRCRLCDEHGLEVEINC 119
QY 116 TLQNTCKCKPDPYCDSPGCEHCVCASCHEGTLEPCTATSNTRCKQSPRNL-WLLT 174
DB 120 TRQNTCKRCNPFNCFCNSAVCEHCDPCTCKKHGIEECTLTSTNPKCKEEDSRDLPLWCL 179
QY 175 ILVLLIPLVFIYRKRYKRCWKRRQDDPSRTSSRETIPMNASLSKYIPRIADMTI 234
DB 180 LLLLPVIVVVIKACKRKHKENQGPHESTYLNPEI-AINLSDVLSKYITTIAGMTL 238
QY 235 QEAKKFARENKIEGKIDIMHSDIQTAEQVOLLWCYQSHGKSDAYQDLIKGLKAE 294
DB 239 SQVKDFVRKNGVSEAKIDEIKNDVQDTAEQVOLLRNWYQLHGCKDCACTLIKGLTAD 298
QY 295 CRTLDKFDQVQKLGKSTPDGTGNEG 323
DB 299 LCTLAEKIHAVILKDI---TSDTENSNGF 324

RESULT 6
Q9TV79
ID Q9TV79 PRELIMINARY; PRT; 319 AA.
AC Q9TV79
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE B-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RP Isono T., Tanbe Y., Nagano Y., Seto A.;
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Db 1 MLGIWTLTLLVLKFLGLSISVNAQVTDINPKGLELRKTVTAJETONLEDOYVGFCHK 60
QY 58 PCOPGKKKVEDCKMNGGTPTCAPCTEGKYMKNHYADKRCRCTLCDDEHGLEVEYNCTL 117
Db 61 PCSPGKKKARDCTVDGDEPCVQCGKEVTDKSHSPKRCRCRLCDDEHGLEVEYNCTR 120
QY 118 TQNTKCKCKPDFDYCDSPGCEHCVRASCCEHGLETPCTATSNTRCKQSPR-NRLWLLTIL 176
Db 121 TQNTKCRCPNFCNSAVCEHCDPCTCBGHIKECSLTSNAKCKEGRANLLWLLCL- 179
QY 177 VLIP-LVFIYKRYKRRKCKWRQDDPESRTSSRETIIPNANSLSKYIPRIAEADMTIQ 235
Db 180 -LLVPILLIIVWVIRCKHRRENQGHRESTTINSETPVPMNLSDVLSKYITVIAEHMTIS 238
QY 236 EAKKFARENNIEGKIDEIMHDSIODTAEQVOLLWCYQSHGSDAYODLIGLKKARC 295
Db 239 QVRDFVRKNGVNEAKIDEIKNDNIQDTAEQVOLLRNWYOLHGKDAYDTLLGLKKANL 298
QY 296 RRTLDKFDVMOKDLGKSTPDGTGNE 322
Db 299 TALVEKIQNIIDKSENSNRQNEQ 325

RESULT 2
Q9TSN4
AC Q9TSN4 PRELIMINARY; PRT; 331 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Death receptor Fas (APO-1/CD95).
GN FAS.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20237686; PubMed=10773350;
RA Murayama Y., Terao K., Inoue-Murayama M.;
RT "Molecular cloning and characterization of cynomolgus monkey Fas.";
RL Hum. Immunol. 61:474-485(2000).
DR EMBL; AB031420; BAA83551.1;
DR HSP; P25445; IDDF
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00208; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 331 AA; 37265 MW; 0C617508081B05DF CRC64;

Query Match 46.3%; Score 835; DB 6; Length 331;
Best Local Similarity 49.7%; Pred. No. 3.8e-66;
Matches 165; Conservative 47; Mismatches 112; Indels 8; Gaps 4;

QY 1 MLWIWAVLPLVLGASOLR-----VHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPPCQ 55
Db 1 MLGIWTLPLVT-SVRLSLKCVNAQVTDISSKGFELRKIVTTIETQNLGLHHEGQFC 59
QY 56 COPCPGKKKVEDCKMNGGTPTCAPCTEGKYMKNHYADKRCRCTLCDDEHGLEVEYNCT 115
Db 60 RNPCPPGERKARDCTVNEDEPCVQCGKEVTDKSHSPKRCRCRLCDDEHGLEVEYNCT 119
QY 116 TLTQNTKCKCKPDFDYCDSPGCEHCVRASCCEHGLETPCTATSNTRCKQSPR-NRLWLLT 174
Db 120 TRTQNTKCRCKPNFCNSAVCEHCDPCTCBGHIKECSLTSNAKCKEGRANLLWLLCL- 179

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QY 175 ILVLLIPLVFIYKRYKRRKCKWRQDDPESRTSSRETIIPNANSLSKYIPRIAEADMTI 234
Db 180 LLLIIPPIVVIWIKKACRKHRENQGHPESTTLNPET-AINLSDVLSKYITTIAGAWTL 238
QY 235 QEAKFARENNIEGKIDEIMHDSIODTAEQVOLLWCYQSHGSDAYODLIGLKKAE 294
Db 239 SQVKDFVRKNGVNEAKIDEIKNDNIQDTAEQVOLLRNWYOLHGKDKADCTLLIKLKTAD 298
QY 295 CRTLDKFDVMOKDLGKSTPDGTGNEQCL 326
Db 299 LCTLAEKIHAVILKIDTSDTENSFRNEIOSL 330

RESULT 3
Q9XS29
ID Q9XS29 PRELIMINARY; PRT; 320 AA.
AC Q9XS29;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE C-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021299; BAA78431.1;
DR EMBL; AB021296; BAA78428.1;
DR HSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 320 AA; 36102 MW; DA235E243220FFB3 CRC64;

Query Match 46.0%; Score 829.5; DB 6; Length 320;
Best Local Similarity 50.3%; Pred. No. 1.1e-65;
Matches 169; Conservative 43; Mismatches 97; Indels 27; Gaps 7;

QY 1 MLWIWAVLPLVLGASOLRVLHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPPCQPCQ 60
Db 1 MTGIWVLLPLIL-----TCIAGSLSTINDCKIKNETQYSTG---YLSGNFCCQLCP 49
QY 61 PGKKKVEDCKMNGGTPTCAPCTEGKYMKNHYADKRCRCTLCDDEHGLEVEYNCTLTQ 120
Db 50 PGTKKADCTSNEGKPDCEPCQEGEEVTDKSHSPKRCRCRLCDDEHGLEVEYDCTIQ 109
QY 121 TKCKCPDFDYCDSPGCEHCVRASCCEHGLETPCTATSNTRCKQ-----SPRNLWLLTI 175
Db 110 TKCRCSNFCNALKEHCDPCTCBGHIKECSLTSNAKCKEGRANLLWLLCL 169
QY 176 LVLLIPLVFIYKRYKRRKCKWRQDDPESRTSSRETIIPNANSLSKYIPRIAEADMTIQ 235
Db 170 L-LLIPIVIGLRRYKRRKCKWRQDDPESRTSSRETIIPNANSLSKYIPRIAEADMTIQ 235
QY 236 EAKKFARENNIEGKIDEIMHDSIODTAEQVOLLWCYQSHGSDAYODLIGLKKAE 295
Db 227 EVKEFVRKNGVNEAKIDEIKNDNIQDTAEQVOLLRNWYOLHGKDKADCTLLIKLKTAD 286
QY 296 RRTLDKFDVMOKDLGKSTPDGTGNE-----ENEGQCL 326
Db 287 CALAEKIQDIQVKDI---TSDHNDLDIRDEKERQSL 319

```

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:00:40 ; Search time 28.6495 Seconds
(without alignments)
2351.779 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWIWAVLPLVLAGSQLRVH.....KDLGKSTPTDGNENEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTEMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	839.5	46.5	328	6 Q9BDP0	Q9bdp0 aotus trivi
2	835	46.3	331	6 Q9TSN4	Q9tsn4 macaca fasc
3	829.5	46.0	320	6 Q9XS29	Q9xs29 oryctolagus
4	825.5	45.8	331	6 Q9BDN0	Q9bdn0 macaca neme
5	822.5	45.6	333	6 Q9BDP2	Q9bdp2 macaca mula
6	820	45.5	319	6 Q9TV79	Q9tv79 oryctolagus
7	816.5	45.3	331	6 Q9BDN4	Q9bdn4 cercocobus
8	815	45.2	334	6 Q9GL40	Q9gl40 macaca mula
9	802.5	44.5	331	6 Q9GK36	Q9gk36 macaca assa
10	802	44.5	327	6 Q97491	Q97491 ovis aries
11	768	42.6	310	6 Q9GK28	Q9gk28 macaca arct
12	609.5	33.8	150	11 Q9R230	Q9r230 rattus norv
13	520.5	28.9	263	6 Q9XS60	Q9xs60 oryctolagus
14	438	24.3	312	13 Q9DGH8	Q9dgh8 gallus gall
15	428.5	23.8	285	13 Q9DGH7	Q9dgh7 gallus gall
16	416	23.1	147	6 Q8SQ52	Q8sq52 felis silve

17	380.5	21.1	124	6 Q8SQ51	Q8sq51 felis silve
18	242.5	13.4	357	13 Q9DF34	Q9df34 brachydanio
19	240	13.3	65	6 Q8SQ49	Q8sq49 felis silve
20	228.5	12.7	438	13 Q9DFV0	Q9dfv0 brachydanio
21	205.5	11.4	283	6 Q9XS28	Q9xs28 cercopithec
22	202.5	11.2	276	13 Q9DD2	Q9dd2 gallus gall
23	198.5	11.0	267	6 Q02764	Q02764 oryctolagus
24	197	10.9	387	13 Q9PVD4	Q9pvd4 xenopus lae
25	179.5	10.0	368	13 Q9IAR7	Q9iar7 gallus gall
26	179.5	10.0	401	13 Q9PRG7	Q9prg7 xenopus lae
27	178.5	9.9	387	11 Q8VD70	Q8vd70 mus musculu
28	177.5	9.8	368	13 Q9FW79	Q9fw79 gallus gall
29	174	9.6	326	12 Q57122	Q57122 cowpox viru
30	172	9.5	351	12 Q73559	Q73559 cowpox viru
31	170	9.4	169	11 Q9JKE0	Q9jke0 rattus norv
32	170	9.4	413	11 Q99MM1	Q99mm1 mus musculu
33	168.5	9.3	347	12 Q57119	Q57119 cowpox viru
34	168.5	9.3	349	12 Q57305	Q57305 cowpox viru
35	168.5	9.3	351	12 Q57121	Q57121 cowpox viru
36	168.5	9.3	360	12 Q57118	Q57118 cowpox viru
37	168	9.3	349	12 Q57098	Q57098 camelpox vi
38	168	9.3	349	12 Q8UYA7	Q8uya7 camelpox vi
39	168	9.3	349	12 Q57284	Q57284 camelpox vi
40	168	9.3	351	12 Q57117	Q57117 cowpox viru
41	167.5	9.3	347	12 Q57115	Q57115 cowpox viru
42	167.5	9.3	355	12 Q85308	Q85308 cowpox viru
43	165.5	9.2	350	12 Q57123	Q57123 cowpox viru
44	165	9.1	326	12 Q57120	Q57120 cowpox viru
45	165	9.1	349	12 Q57111	Q57111 variola vir

ALIGNMENTS

RESULT 1

Q9BDP0 ID Q9BDP0 PRELIMINARY; PRT; 328 AA.

AC Q9BDP0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE FAS antigen CD95.

OS Aotus trivirgatus (Night monkey) (Douroucoul).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=9505;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21383618; PubMed=11491535;

RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,

RA Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing, and homology analysis of nonhuman primate

RT Fas/Fas-ligand and co-stimulatory molecules."

RL Immunogenetics 53:315-328(2001).

DR EMBL; AF344835; AAK37531.1; -;

DR HSSP; P25445; IDDF.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR_c6; 2.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS50017; DEATH DOMAIN; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00050; TNFR_NGFR_2; 2.

FT VARIANT 157 157 S->T.

SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;

Query Match 46.5%; Score 839.5; DB 6; Length 328;

Best Local Similarity 50.2%; Pred. No. 1.5e-66;

Matches 164; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

QY 1 MLWIWAVLPLVL---AGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQ 57

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:58:17 ; Search time 15.3127 seconds
(without alignments)
885.720 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWIAVPLVLAGSQLRVH.....KDLGKSTPDGTGNEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	327	1	TNR6_MOUSE
2	1058.5	58.7	324	1	TNR6_RAT
3	856	47.5	335	1	TNR6_HUMAN
4	841.5	46.6	332	1	TNR6_PIG
5	814	45.1	323	1	TNR6_BOVIN
6	272	15.1	381	1	T10B_MOUSE
7	215	11.9	468	1	T10A_HUMAN
8	205	11.4	176	1	TR23_MOUSE
9	205	11.4	283	1	TR14_HUMAN
10	203.5	11.3	271	1	TNR4_RAT
11	202	11.2	272	1	TNR4_MOUSE
12	196	10.9	417	1	TR12_HUMAN
13	194.5	10.8	277	1	TNR5_HUMAN
14	189.5	10.5	455	1	TR1A_HUMAN
15	185	10.3	454	1	TR1A_MOUSE
16	183	10.1	180	1	TR22_MOUSE
17	179.5	10.0	435	1	TNR3_HUMAN
18	179.5	10.0	440	1	T10B_HUMAN
19	179	9.9	461	1	TR1A_RAT
20	178	9.9	260	1	TNR7_HUMAN
21	172	9.5	351	1	CRMB_COMPX
22	171	9.5	277	1	TNR4_HUMAN
23	169	9.4	461	1	TR1A_PIG
24	168	9.3	349	1	CRMB_CAMPS
25	167	9.3	250	1	TNR7_MOUSE
26	166.5	9.2	386	1	T10D_HUMAN
27	165.5	9.2	416	1	TR16_CHICK
28	165	9.1	289	1	TNR5_MOUSE
29	163	9.0	259	1	T10C_HUMAN
30	163	9.0	349	1	CRMB_VARV
31	161	8.9	471	1	TR1A_BOVIN
32	155.5	8.6	269	1	TNR5_BOVIN
33	155.5	8.6	300	1	TR6B_HUMAN

34	154.5	8.6	425	1	TR16_RAT
35	154.5	8.6	595	1	TNR8_HUMAN
36	154	8.5	415	1	TNR3_MOUSE
37	148	8.2	461	1	TR1B_HUMAN
38	144	8.0	401	1	T11B_HUMAN
39	144	8.0	401	1	T11B_RAT
40	143	7.9	401	1	TR1B_MOUSE
41	143	7.9	417	1	TR16_MOUSE
42	141	7.8	427	1	TR16_HUMAN
43	139	7.7	297	1	XEDA_HUMAN
44	128.5	7.1	616	1	TR11_HUMAN
45	127.5	7.1	687	1	VS41_GIALA

ALIGNMENTS

RESULT 1

ID	TNR6_MOUSE	STANDARD;	PRT;	327 AA.
AC	P25446; O9DC01;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DE	Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).			
GN	TNFRSF6 OR APT1 OR FAS.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-92148151; PubMed-1371136;			
RA	Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,			
RA	Copeland N.G., Jenkins N.A., Nagata S.;			
RT	"The cDNA structure, expression, and chromosomal assignment of the mouse Fas antigen."			
RL	J. Immunol. 148:1274-1279(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129/SV;			
RK	Koczan D., Ibrahim S.M., Thiesen H.J.;			
RT	"Role of a mutant fas receptor in a transgenic mouse."			
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBAJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6J; TISSUE-Kidney;			
RK	MEDLINE-21085660; PubMed-11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 405:685-690(2001).			
RN	[4]			
RP	SEQUENCE OF 1-96 FROM N.A.			
RX	MEDLINE-93189576; PubMed-7680478;			

P07174	rattus norv
P28908	homo sapien
P50284	mus musculus
P20333	homo sapien
O00300	homo sapien
O08727	rattus norv
O08712	mus musculus
Q920W1	mus musculus
P08138	homo sapien
Q9hav5	homo sapien
Q9y6q6	homo sapien
P92127	giardia lam

RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
 RT "Aberrant transcription caused by the insertion of an early
 RT transposable element in an intron of the Fas antigen gene of lpr
 RL mice.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
 RN [5]
 RP VARIANT LPR
 RX MEDLINE-92195401; PubMed-1372394;
 RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
 RA Nagata S.;
 RT "Lymphoproliferation disorder in mice explained by defects in Fas
 RT antigen that mediates apoptosis.";
 RL Nature 356:314-317(1992).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
 CC LIVER, LUNG, HEART, AND ADULT OVARY.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- DISEASE: DEFECS IN TNFSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
 CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
 CC PRODUCTION.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 DR EMBL; M83649; AAA37593.1; -
 DR EMBL; AK002590; BAB22211.1; -
 DR EMBL; AJ295702; CAC00638.1; -
 DR EMBL; AJ295703; CAC00638.1; JOINED.
 DR EMBL; AJ295704; CAC00638.1; JOINED.
 DR EMBL; S56490; AAB25700.1; -
 DR EMBL; S56485; AAB25700.1; JOINED.
 DR EMBL; S56486; AAB25700.1; JOINED.
 DR PIR; A46484; A46484.
 DR HSP; P25445; 1DDF.
 DR MGD; MGI:95484; Tnfrsf6.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001388; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR Pfam; PF00531; death; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Disease mutation.
 FT SIGNAL 1 21
 FT CHAIN 22 327
 FT DOMAIN 22 169
 FT TRANSMEM 170 186
 FT DOMAIN 187 327
 FT REPEAT 43 79
 FT REPEAT 80 123
 FT REPEAT 124 162
 FT REPEAT 222 306
 FT DOMAIN 44 55
 FT DISULFID BY SIMILARITY.

FT DISULFID 56 69 BY SIMILARITY.
 FT DISULFID 59 78 BY SIMILARITY.
 FT DISULFID 81 97 BY SIMILARITY.
 FT DISULFID 100 115 BY SIMILARITY.
 FT DISULFID 103 123 BY SIMILARITY.
 FT DISULFID 125 139 BY SIMILARITY.
 FT DISULFID 142 153 BY SIMILARITY.
 FT DISULFID 145 161 BY SIMILARITY.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 246 246 I -> N (IN LPR).
 FT CONFLICT 38 38 H -> R (IN REF. 3).
 SQ SEQUENCE 327 AA; 37418 MW; F6BFC5ACE356EEE CRC64;
 Query Match 100.0%; Score 1804; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1e-133;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISLKLRRVHETDKNCSGLYQGGPCCPCQ 60
 DB 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISLKLRRVHETDKNCSGLYQGGPCCPCQ 60
 QY 61 PGKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN 120
 DB 61 PGKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN 120
 QY 121 TKCKCKPDFCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRNLWLLTILVLI 180
 DB 121 TKCKCKPDFCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRNLWLLTILVLI 180
 QY 181 PLVFIYKRYKRCWKRRQDDPSRTSSRETIPMNASNLSKYIPRIADMTIOEAKKF 240
 DB 181 PLVFIYKRYKRCWKRRQDDPSRTSSRETIPMNASNLSKYIPRIADMTIOEAKKF 240
 QY 241 ARENNKEGIDEIMHDSIODTAEQVQLLLCWYQSHGSKSDAYQDILKGLKAECRRTLD 300
 DB 241 ARENNKEGIDEIMHDSIODTAEQVQLLLCWYQSHGSKSDAYQDILKGLKAECRRTLD 300
 QY 301 KFDQVMQKDLGKSTPDPTGNEGQCLE 327
 DB 301 KFDQVMQKDLGKSTPDPTGNEGQCLE 327
 RESULT 2
 TNFR6_RAT
 ID TNFR6_RAT STANDARD; PRT; 324 AA.
 AC Q63199;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
 DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
 DE (CD95).
 GN TNFRSF6 OR PT1 OR FAS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE-94128114; PubMed-7507668;
 RA Kimura K., Yamamoto M., Wakatsuki T.;
 RT "A variant mRNA species encoding a truncated form of Fas antigen in
 RT the rat liver.";
 RL Biochem. Biophys. Res. Commun. 198:666-674(1994).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or

RA MEDLINE-95300225; PubMed-7540117;
 RA Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,
 RA Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;
 RT "Dominant interfering Fas gene mutations impair apoptosis in a human
 RT autoimmune lymphoproliferative syndrome.";
 RL Cell 81:935-946(1995).
 RN [9]
 RP VARIANT ALPS TYR-260.
 RX MEDLINE-97066823; PubMed-8929361;
 RA Drappa J., Vaishnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;
 RA "Fas gene mutations in the Canale-Smith syndrome, an inherited
 RT lymphoproliferative disorder associated with autoimmunity.";
 RL New Engl. J. Med. 335:1643-1649(1996).
 RN [10]
 RP VARIANT ALPS TRP-121 AND CYS-232.
 RX MEDLINE-97180145; PubMed-9028321.
 RA Bettinardi A., Brugnani D., Quiros-Roldan E., Malagoli A.,
 RA La Grutta S., Correria A., Notarangelo L.D.;
 RT "Missense mutations in the Fas gene resulting in autoimmune
 RT lymphoproliferative syndrome: a molecular and immunological
 RT analysis.";
 RL Blood 89:902-909(1997).
 RN [11]
 RP VARIANT ALPS ASP-257 AND SER-310.
 RX MEDLINE-97180739; PubMed-9028957;
 RA Sneller M.C., Wang J., Dale J.K., Strober W., Middleton L.A., Choi Y.,
 RA Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,
 RA Straus S.E.;
 RT "Clinical, immunologic, and genetic features of an autoimmune
 RT lymphoproliferative syndrome associated with abnormal lymphocyte
 RT apoptosis.";
 RL Blood 89:1341-1348(1997).
 RN [12]
 RP VARIANT ALPS ALA-28.
 RX MEDLINE-97463833; PubMed-9322534;
 RA Pensati L., Costanzo A., Ianni A., Accapezzato D., Torio R.,
 RA Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,
 RA Levrero M.;
 RT "Fas/Apo1 mutations and autoimmune lymphoproliferative syndrome in a
 RT patient with type 2 autoimmune hepatitis.";
 RL Gastroenterology 113:1384-1389(1997).
 RN [13]
 RP VARIANT ALPS VAL-260.
 RX MEDLINE-99038860; PubMed-9821419;
 RA Infante A.J., Britton H.A., DeNapoli T., Middleton L.A., Lenardo M.J.,
 RA Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;
 RT "The clinical spectrum in a large kindred with autoimmune
 RT lymphoproliferative syndrome caused by a Fas mutation that impairs
 RT lymphocyte apoptosis.";
 RL J. Pediatr. 133:629-633(1998).
 RN [14]
 RP VARIANT ALPS LYS-241 AND GLN-250.
 RX MEDLINE-99192346; PubMed-10090885;
 RA Jackson C.E., Fleisher R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,
 RA Dale J.K., Fleisher T.A., Middleton L.A., Sneller M.C., Lenardo M.J.,
 RA Straus S.E., Puck J.M.;
 RT "Autoimmune lymphoproliferative syndrome with defective Fas: genotype
 RT influences penetrance.";
 RL Am. J. Hum. Genet. 64:1002-1014(1999).
 RN [15]
 RP VARIANT ALPS GLY-272.
 RX MEDLINE-99270228; PubMed-10340403;
 RA Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B.,
 RA Gahr M., Roesler J.;
 RT "Defective apoptosis due to a point mutation in the death domain of
 RT CD95 associated with autoimmune lymphoproliferative syndrome, T-cell
 RT lymphoma, and Hodgkin's disease.";
 RL Exp. Hematol. 27:868-874(1999).
 RN [16]
 RP VARIANT ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.
 RX MEDLINE-99126461; PubMed-9927496;
 RA Vaishnaw A.K., Orlicki J.R., Chu J.-L., Krammer P.H., Chao M.V.,
 RA Elkon K.B.;

RT "The molecular basis for apoptotic defects in patients with CD95
 RT (Fas/Apo-1) mutations.";
 RL J. Clin. Invest. 103:355-363(1999).
 RN [17]
 RP VARIANT NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;
 RX VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.
 RA MEDLINE-99005325; PubMed-9787134;
 RA Groenbaek K., Straten P.T., Rafikier E., Ahrenkiel V., Andersen M.K.,
 RA Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;
 RT "Somatic Fas mutations in non-Hodgkin's lymphoma: association with
 RT extranodal disease and autoimmunity.";
 RL Blood 92:3018-3024(1998).
 RN [18]
 RP VARIANT ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.
 RX MEDLINE-97180145; PubMed-9028321;
 RA Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,
 RA Roosen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
 RA Fischer R.E., Jackson C.E., Lin A.Y., Baemler C., Siegert E.,
 RA Marx A., Vaishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;
 RT "The development of lymphomas in families with autoimmune
 RT lymphoproliferative syndrome with germline Fas mutations and
 RT defective lymphocyte apoptosis.";
 RL Blood 98:194-200(2001).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both. The secreted isoforms 2 to 6 block apoptosis (in vitro).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC Secreted (isoforms 2 to 6).
 CC -1- ALTERNATIVE PRODUCTS: 6 isoforms; 1 (shown here), 2/Del2/d,
 CC 3/Del3/e, 4/b, 5/c and 6/TMDel/a; are produced by alternative
 CC splicing.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- DISEASE: Defects in TNFSF6 are a cause of autoimmune
 CC lymphoproliferative syndrome (ALPS), also known as Canale-Smith
 CC syndrome (CSS), a childhood syndrome involving hemolytic anemia
 CC and thrombocytopenia with massive lymphadenopathy and
 CC splenomegaly.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- DATABASE: NAME-PRO; NOTE-CD guide CD95 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd95.htm".
 CC -----
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 CC -----
 CC EMBL; M67454; AAA63174.1; -
 CC EMBL; X63717; CAA45250.1; -
 CC EMBL; X89101; CAA61473.1; -
 CC EMBL; 247993; CAA88031.1; -
 CC EMBL; 247994; CAA88032.1; -
 CC EMBL; 247995; CAA88033.1; -
 CC EMBL; 270520; CAA94431.1; -

Query Match

47.5%; Score 856; DB 1; Length 335;

Best Local Similarity 49.4%; Pred. No. 9e-60;

Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIAVPLVLVLAG-----SQLRVHTQGTNSISLSKLRVRVHETDKNCSEGLYQGPFCC 56

Db 1 MLGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLERKTVTTVTQNLGLHHDGQFCH 60

QY 57 QPCQPGKKVDECKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCILCDEEHLEVTNCT 116

Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHSSKRCRLCDGEGHVEINCT 120
QY 117 LQNTCKCKPDPYCDSPGCEHCVCASCHEGTLFECTATSNCRKQSPRNLWLLTIL 176
Db 121 RYNTCKRCKPFPFCNFCSTGCHGDCPTCKEHLKECTLTSTNTKCEBGRSLNGLWCLL 180
QY 177 VLLIPL-VFIYKRYKRRKWKRRQDDP---ESRTSSRETIPMNASNLISLSKYIPRIAE 232
Db 181 LLPIPLVVKRKEVCKTKRKHENQSGSHESPTLNPETVAINLSVDLSKYITTAGVM 240
QY 233 TIOEAKFFARENNIKGKIDEIMHDSIQDTAEQVOLLWCWYQSHGSKSDAYQDLIKGLK 292
Db 241 TISQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHLGKKEAYDTLIDKLLK 300
QY 293 AECRRTLDFQDMVKDLKSPDPTGNEGQCL 326
Db 301 ANLCTLAETIQTILADITSDSSENFRNEIQSL 334

RESULT 4

TNR6_PIG
ID TNR6_PIG STANDARD; PRT; 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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or send an email to license@isb-sib.ch).

DR EMBL; AJ200120; CAA04596.1; -
DR HSP; P25445; IDDF
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR Pfam: PF00531; death; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.

DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 332 TUMOR NECROSIS FACTOR RECEPTOR
FT 17 332 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 17 175 POTENTIAL.
FT TRANSMEM 176 192 SUPERFAMILY MEMBER 6.
FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).
FT REPEAT 45 81 TNFR-CYS 1.
FT REPEAT 82 125 TNFR-CYS 2.
FT REPEAT 126 164 TNFR-CYS 3.
FT DOMAIN 227 311 DEATH.
FT DISULFID 46 57 BY SIMILARITY.
FT DISULFID 58 71 BY SIMILARITY.
FT DISULFID 61 80 BY SIMILARITY.
FT DISULFID 83 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 141 BY SIMILARITY.
FT DISULFID 144 155 BY SIMILARITY.
FT DISULFID 147 163 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 332 AA; 37592 MW; 5B8B03682756BF1B CRC64;
Query Match 46.6%; Score 841.5; DB 1; Length 332;
Best Local Similarity 49.0%; Pred. No. 1.2e-58;
Matches 164; Conservative 50; Mismatches 108; Indels 13; Gaps 6;
QY 1 MLWIAVLPLV---LAGSQLR-VHTQGTNSISESLKLRVRVHEPDKNCSEGLYGGPFCC 56
Db 1 MSGIWLILLSVFTCIAGPLSKGDDAQVTPDSEMKL--NITRESECEPQHQREGQFCC 58
QY 57 QPCQPKKKVEDCKMNGGTPTCAPTEGKEYMDKNHVDKRCRTCLDEEHGLEVEINCT 116
Db 59 QPCPPGKRKHADCTSPGGAPQCPVCEGDTDKNHSSKRCRCVDCGEGHGLEVEINCT 118
QY 117 LTQNTCKCKPDPYCDSPGCEHCVCASCHEGTLFECTATSNCRK-----QSPRNLW 171
Db 119 RTQNTCKCKPDPYCDSPGCEHCVCASCHEGTLFECTATSNCRKVFQSGRSNLHW 178
QY 172 LLTILVLLPLVFIYKRYKRRKWKRRQDDPESRTSSRETIPMNASNLISLSKYIPRIAE 231
Db 179 LWALLILIPALVYREV-KRRCRKENGQYKPTTSNAEEVPM-IKDVLDLKGITRIAEQ 236
QY 232 MTIOEAKFFARENNIKGKIDEIMHDSIQDTAEQVOLLWCWYQSHGSKSDAYQDLIKGLK 291
Db 237 MKITEVKDFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHLGKKEAYDTLIDKLLR 296
QY 292 KACRRTLDFQDMVKDLKSPDPTGNEGQCL 326
Db 297 KAKLSALADKINDIVQKDVTSQENANSQNESESL 331

RESULT 5

TNR6_BOVIN
ID TNR6_BOVIN STANDARD; PRT; 323 AA.
AC PS1867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96226401; PubMed=8634151;

YOO J., Stone R.T., Beattie C.W.;
 "Cloning and characterization of the bovine Fas.";
 DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC tolerance, apoptosis may have a role in the induction of peripheral
 CC both (By similarity).
 CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U34794; AAC48546.1; .
 CC HSSP; P25445; 1DDF.
 CC InterPro; IPR000488; Death.
 CC InterPro; IPR001388; TNFR_C6.
 CC Pfam; PF00020; TNFR_C6; 3.
 CC Pfam; PF00531; death; 1.
 CC SMART; SM00005; DEATH; 1.
 CC SMART; SM00208; TNFR; 3.
 CC PROSITE; PS00652; TNFR_NGFR_1; 2.
 CC PROSITE; PS00652; TNFR_NGFR_2; 2.
 CC PROSITE; PS00500; TNFR_NGFR_2; 2.
 CC PROSITE; PS00500; TNFR_NGFR_2; 2.
 CC Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
 CC SIGNAL 1 16 POTENTIAL.
 CC CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
 CC SUPERFAMILY MEMBER 6
 CC
 CC DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 171 188 POTENTIAL.
 CC DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
 CC REPEAT 45 80 TNFR-CYS 1.
 CC REPEAT 81 124 TNFR-CYS 2.
 CC REPEAT 125 163 TNFR-CYS 3.
 CC DOMAIN 238 306 DEATH.
 CC DISULFID 45 56 BY SIMILARITY.
 CC DISULFID 57 70 BY SIMILARITY.
 CC DISULFID 60 79 BY SIMILARITY.
 CC DISULFID 82 98 BY SIMILARITY.
 CC DISULFID 101 116 BY SIMILARITY.
 CC DISULFID 104 124 BY SIMILARITY.
 CC DISULFID 126 140 BY SIMILARITY.
 CC DISULFID 143 154 BY SIMILARITY.
 CC DISULFID 146 162 BY SIMILARITY.
 CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 323 AA; 36445 MW; 4D88A90E91F4892 CRC64;

Query Match

45.1%; Score 814; DB 1; Length 323;

Best Local Similarity 49.1%; Pred. No. 1.6e-56;

Matches 164; Conservative 49; Mismatches 101; Indels 20; Gaps 8;

QY 1 MLWIAVPLV---LAGSQLR---VHTQNTSISLSKLRVHETDKN-CEGLYQGGP 53
 DB 1 MSGIWHLSLFTISVSGPLSKGENAHAGIN--SEGLK-----NITEANSQEGLYREHQ 54
 QY 54 FCQCPQCPGKKVDECKMNGGPTCAPCTCEKEYMDKNHYADKRCRTLCDEHGLEVET 113
 DB 55 FCQCPQCPGKNGKDCRGDTPCEVLCSEGNEYTDKSHSHSKRCISCDHEHGLEVBQ 114
 QY 114 NCTLTONTCKCKPDPYCDSPGCEHCVRCAECSEHGTLEPCTATNTNCR-KQSPRNLWL 172

DB 115 NCTRTNTRKCRCKSNFFCNSPCEHCNPTCTCEHGIIEKCTPTSTNCKGSRSHANLWA 174
 QY 173 LTLVLLPLVFTYRKYRKKWKRRQDDPESRTSSRETIPMNASNLSLSKYPRIAEOM 232
 DB 175 L--LILLIPVLIYVVKRSRERNKNDYCSAASNDGRLNLTVDLGLKYPSTAEOM 232
 QY 233 TIOEAKFARENNIKGKIDEMHDSIQDTAEOKVOLLICWYOSHGSKSDAYODLIGLKK 292
 DB 233 RITEVEKFEYRKNMGMEAKIDIMHNDVHETAEOKVOLLRNWYQSHGKNAYCTLTSLPK 292
 QY 293 AECRRRLDFQDMVQKDLGKSTPDTGNEGQCL 326
 DB 293 A----LAEKICDIVMKDITNERENANLQNEENL 322
 RESULT 6
 ID T10B.MOUSE STANDARD; PRT; 381 AA.
 AC Q9QZM4; Q9JUL5; Q9JUL6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 10B precursor (Death
 DE receptor 5) (MK).
 GN TNFRSF10B OR DR5 OR KILLER.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=99310501; PubMed=10383128;
 RA Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
 RT "Molecular cloning and functional analysis of the mouse homologue of
 RT the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand
 RT (TRAIL) death receptor";
 RL Cancer Res. 59:2770-2775(1999).
 RP [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Nakamura Y., Tamari M., Watanabe O.;
 RT "Mouse TRAIL receptor";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
 CC adaptor molecule FADD recruits caspase-8 to the activated
 CC receptor. The resulting death-inducing signaling complex (DISC)
 CC performs caspase-8 proteolytic activation which initiates the
 CC subsequent cascade of caspases (aspartate-specific cysteine
 CC proteases) mediating apoptosis. Promotes the activation of NF-
 CC kappaB.
 CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
 CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC
 CC EMBL; AF176833; AAD52656.1; .
 CC EMBL; AB031081; BAA96462.1; .
 CC EMBL; AB031082; BAA96463.1; .
 CC HSSP; O14763; 1DOG.
 CC MGI; MGI:1341090; Tnfrsf10b.


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FT REPEAT 147 188
FT REPEAT 189 229
FT DOMAIN 365 448
FT POLY-ALA 29 32
FT DISULFID 132 145
FT DISULFID 148 164
FT DISULFID 167 180
FT DISULFID 170 188
FT DISULFID 190 204
FT DISULFID 207 221
FT DISULFID 211 229
FT CARBOHYD 156 156
FT CONFLICT 141 141
FT CONFLICT 209 209
SQ SEQUENCE 468 AA; 50061 MW; 7E9661859A550CD4 CRC64;

Query Match
Best Local Similarity 21.1%; Score 215; DB 1; Length 468;
Matches 82; Conservative 64; Mismatches 137; Indels 106; Gaps 16;

QY 13 AGSLRVH-----TGTNISESLKLRVRHETDKNCKSEGLYQGGFFCCQPCQ 61
DB 82 ASPLRVHKTKEVVVGVLLQVPSAATIKLH-----DQSGTQWEHSP-L-GE 134
QY 62 GKXVEDCKMGGTPTCAPCTEGKEYMDKNHYADKRCRTLCDEHGLEVETNCTLTQ 121
DB 135 GSHSEH-----PGACNRCCTEGVYTNASNNLFCALPCTACKSDE--EERS 186
QY 122 KCKKPDFYCDSPGCEHCVRCA--SCEHG--TLEPCTATSTNCC--RKQSPNRLW 176
DB 187 ACQCKPGFTNRDNDNAEMCRKSCGPRGWVVKDCTPWSIDIECVKHSNGHNTW 246
QY 177 VLLPLVFIY-----RKYRKCKWKR--RQDDPSRTSSRETIPMNASNL 219
DB 247 TLVPLLVAVLVVCCIGSGCGDPRKMDRVCFWRLGRLGPGAEDNAHNEILLN 306
QY 220 S-----LSKYIPRIADMTIQ-----EAK----- 238
DB 307 STFFSEQMESQEPADLTGVTVPGFGEAQLLGPAAEGSQRRLLVPANGADPT 366
QY 239 ---KFA-----RNNIKGKIDIMHDSIODTAEQVKVQLLWYQSHGSKDAY 283
DB 367 FFDKFAVTPDSDWQMLRQLDLTKNEID--VVRAGTAGPDGALYAMLKMKVNT 425
QY 284 QDLTKGLKAPCRRTLKDFQDMVKQDLGK 312
DB 426 HTLLDALERMEERHAKEIKQDLL--VDSGK 453

RESULT 8
TR23_MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q9VHC0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN TNFRSF23 OR TNFRSF11 OR TNFRH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN-129/Sv; TISSUE-Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region: Implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2491-2706(2000).
RN [2]

```

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RP SEQUENCE FROM N.A.
RA Pan G., Mao W., Rissler P.;
RL "Characterization of SOB, a member of the TNFR family.";
CC Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -|- TISSUE SPECIFICITY: Ubiquitous
CC -|- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL; AJ278264; CAC16405.1; -
DR EMBL; AJ276505; CAC27352.1; -
DR EMBL; AY046550; AAL05072.1; -
DR HSSP; P19438; 1EXT.
DR MGD; MGI:1930269; Tnfrsf23.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 9
FT TRANSMEM 10 30
FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 176
FT REPEAT 37 72
FT REPEAT 74 114
FT REPEAT 115 155
FT DISULFID 38 49
FT DISULFID 50 63
FT DISULFID 53 72
FT DISULFID 75 90
FT DISULFID 93 106
FT DISULFID 96 114
FT DISULFID 116 131
FT DISULFID 134 147
FT DISULFID 137 155
FT CARBOHYD 148 148
SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DBD7D CRC64;

Query Match
Best Local Similarity 11.4%; Score 205; DB 1; Length 176;
Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps 5;

QY 43 NCSEGLYQGGPCCQPCQPKKKKVEDCKMNGGTPPTCAPCTEGKEYMDKNHYADKRCR 102
DB 37 NCPDGEYQSDVCCCKTPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKDNGLHDLCLST 95
QY 103 CDEEHGLEVETNCTLTQNTKCKKPD-FYCDSPGCEHCVRCA--TLEPCTATSTNT 159
DB 96 CKDKQNWAD--CSATSDRCKECQIGLYYYDPKFPESCRCPTKCPQGPVLEQCNSTANT 153
QY 160 NCRK--QSPNRNLWLLTILVLLI 180
DB 154 VCSSSVSNPRNWLFLMLLVFCI 176

RESULT 9
TR14_HUMAN STANDARD; PRT; 283 AA.
AC Q92956; Q9UM65; Q96J31; Q8WXR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2) (TR2).
GN TNFRSF14 OR HVEM OR HVEA.

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FT DISULFID 63 77 BY SIMILARITY.
 FT DISULFID 80 95 BY SIMILARITY.
 FT DISULFID 83 103 BY SIMILARITY.
 FT DISULFID 105 123 BY SIMILARITY.
 FT DISULFID 126 139 BY SIMILARITY.
 FT DISULFID 145 164 BY SIMILARITY.
 FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 15 15 A -> G (IN REF. 2).
 SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 11.2%; Score 202; DB 1; Length 272;
 Best Local Similarity 26.5%; Pred. No. 7.3e-09;
 Matches 69; Conservative 22; Mismatches 85; Indels 84; Gaps 12;

QY 2 LNIWAVLPLVLAGSQLRVHTQGTNSISESLKLRVRVETDKNCSGLYQGGPFCQPCQP 61
 DB 1 MYVWVQOPTALL---LLALITGVTA-----RRL-----NCVKHTYPSGHKCCRECQP 44
 QY 62 GKKVDECKNGGPTCAPCTEGKEYMDKNHYADKRCRTLCDEHGLEVTNCTLTQNT 121
 DB 45 GHGMVSRCDHTRDT-LCHPCETG-FYNEAVNY-DTCRQCTQCNHRSGSELKQNCPTQDT 101
 QY 122 KCKKPDFY-----CD---SPG---CEHCVRG----- 142
 DB 102 VCRPGCTQPRDQSGYKLGVDVCPGPHFSPGNACKPWNTCTLSGKQTRHPASDGLD 161
 QY 143 ASCE-----HGTLEPCATSTNCRKQS-----PRNLWLTLTIL 176
 DB 162 AVCEDRSLLATLWETQRTFRPTTVQSTTWPRTELSPPTLTPGPAFVLLGLGL 221
 QY 177 VLLIPLVFIYKRYKRCWK 196
 DB 222 GLAPLTVLLALYLLKAWR 241

RESULT 12

TR12_HUMAN
 ID TR12_HUMAN STANDARD; PRT; 417 AA.
 AC Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;
 AC Q99830; Q9BY86; Q14865; Q14866; Q00275; Q00276; Q00277; Q00278;
 AC Q00279; Q00280; Q9UME0; Q9UME1; Q9UME5;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 12 precursor
 DE (WSL-1 protein) (Apoptosis-inducing receptor DR3) (Apoptosis-
 DE mediating receptor TRAMP) (Death domain receptor 3) (WSL protein)
 DE (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated
 DE receptor of death) (LARD).
 GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
 RC TISSUE=Lymphoid;
 RX MEDLINE=97088617; PubMed=8934525;
 RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
 RA Grinham C.J., Brown R., Farrow S.N.;
 RT "A death-domain-containing receptor that mediates apoptosis.";
 RL Nature 384:372-375(1996).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=97081063; PubMed=8875942;
 RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
 RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
 RT "Signal transduction by DR3, a death domain-containing receptor
 RT related to TNFR-1 and CD95.";
 RL Science 274:990-992(1996).
 [3]
 RN SEQUENCE FROM N.A.

RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Heart;
 RX MEDLINE=97148200; PubMed=8994832;
 RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
 RA Goddard A.D., Bauer K.D., Ashkenazi A.;
 RT "Apo-3, a new member of the tumor necrosis factor receptor family,
 RT contains a death domain and activates apoptosis and NF-kappa-B.";
 RL Curr. Biol. 6:1669-1676(1996).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
 RX MEDLINE=9727273; PubMed=9114039;
 RA Sreaton G.E., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
 RA McMichael A.J., Bell J.I.;
 RT "LARD: a new lymphoid-specific death domain containing receptor
 RT regulated by alternative pre-mRNA splicing.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 [6]
 RN SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
 RX MEDLINE=98113360; PubMed=9446802;
 RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
 RA Salles G.;
 RT "A new death receptor 3 isoform: expression in human lymphoid cell
 RT lines and non-Hodgkin's lymphomas.";
 RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
 [7]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
 RA Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 [8]
 RN SEQUENCE OF 4-417 FROM N.A.
 RC TISSUE=Brain, and Retal lung;
 RX MEDLINE=97205335; PubMed=9052839;
 RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
 RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
 RA Browning J.L., MacDonald H.R., Tschoopp J.;
 RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology
 RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
 RL Immunity 6:79-88(1997).
 [9]
 RN SEQUENCE OF 7-417 FROM N.A.
 RC TISSUE=Brain;
 RX Chaudhary P.M., Hood L.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly
 CC with the adaptor TRADD. Mediates activation of NF-kappaB and
 CC induces apoptosis. May play a role in regulating lymphocyte
 CC homeostasis.
 CC -1- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
 CC THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
 CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
 CC and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
 CC (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 12 ISOFORMS: 1/WSL-1/LARD-1A (SHOWN HERE),
 CC 2/LARD-1B, 3/WSL-S1/LARD-3, 4/WSL-S2/LARD-2, 5/LARD-4/LARD-11,
 CC 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND
 CC 12/BETA SOLUBLE; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
 CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
 CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
 CC -1- PTM: GLYCOSYLATED (PROBABLE).
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine
 CC residue instead of arginine.

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Db 196 VVIPILFIFAILLVLFVFKVAKK 221

RESULT 14

TRIA_HUMAN STANDARD: PRT: 455 AA.

AC P19438;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1A precursor (p50)

DE (TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor

DE binding protein 1 (TNFRI)]

GN TNFRSF1A OR TNFRI OR TNFAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=90235285; PubMed=2158863;

RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,

RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;

RT "Molecular cloning and expression of a receptor for human tumor

RT necrosis factor.";

RT Cell 61:361-370(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=90235284; PubMed=2158862;

RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,

RA Tabuchi H., Lesslauer W.;

RT "Molecular cloning and expression of the human 55 kd tumor necrosis

RT factor receptor.";

RT Cell 61:351-359(1990).

RN [3]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.

RX MEDLINE=91006021; PubMed=1698610;

RA Nohar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,

RA Aderka D., Holtmann H., Wallach D.;

RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA

RT for the type I TNF-R, cloned using amino acid sequence data of its

RT soluble form, encodes both the cell surface and a soluble form of the

RT receptor.";

RL EMBL J. 9:3269-3278(1990).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=9100841; PubMed=1702293;

RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,

RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;

RT "Molecular cloning and expression of human and rat tumor necrosis

RT factor receptor chain (p60) and its soluble derivative, tumor

RT necrosis factor-binding protein.";

RL DNA Cell Biol. 9:705-715(1990).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=91017509; PubMed=2170974;

RA Gray P.W., Barrett K., Chantray D., Turner M., Feldman M.;

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and

RT expression of recombinant soluble TNF-binding protein.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=92250049; PubMed=1315717;

RA Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;

RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and

RT localization to chromosome 12p13.";

RL Genomics 13:219-224(1992).

RN [7]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RA Strausberg R.;

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[8]

RL SEQUENCE OF 41-45.

RN MEDLINE=90110215; PubMed=2153136;

RX Engelmann H., Novick D., Wallach D.;

RT "Two tumor necrosis factor-binding proteins purified from human

RT urine. Evidence for immunological cross-reactivity with cell surface

RT tumor necrosis factor receptors.";

RL J. Biol. Chem. 265:1531-1536(1990).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.

RX MEDLINE=93258809; PubMed=8387891;

RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,

RA Broger C., Loetscher H., Lesslauer W.;

RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF

RT beta complex: Implications for TNF receptor activation.";

RL Cell 73:431-445(1993).

RN [10]

RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.

RX MEDLINE=97094982; PubMed=8939750;

RA Naismith J.H., Devine I.Q., Khono H., Sprang S.R.;

RT "Structures of the extracellular domain of the type I tumor necrosis

RT factor receptor.";

RL Structure 4:1251-1262(1996).

RN [11]

RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.

RX MEDLINE=99213501; PubMed=10199409;

RA McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,

RA Ogunkolade B.W., Centola M., Mansfield E., Gadin M., Karenko L.,

RA Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,

RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,

RA Schlimgen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,

RA Mulvey J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,

RA Hittman G.A., O'Shea J., Kastner D.L.;

RT "Germline mutations in the extracellular domains of the 55 kDa TNF

RT receptor, TNFR1, define a family of dominantly inherited

RT autoinflammatory syndromes.";

RL Cell 97:133-144(1999).

RN [12]

RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric

CC TNFSF1/lymphotxin-alpha. The adaptor molecule FADD recruits

CC caspase-8 to the activated receptor. The resulting death-inducing

CC signaling complex (DISC) performs caspase-8 proteolytic activation

CC which initiates the subsequent cascade of caspases (aspartate-

CC specific cysteine proteases) mediating apoptosis. Contributes to

CC the induction of noncytotoxic TNF effects including anti-viral

CC state and activation of the acid sphingomyelinase.

CC [13] SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO

CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

CC NF-KAPPA B SIGNALING.

CC [14] SUBCELLULAR LOCATION: Type I membrane protein and secreted.

CC [15] DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO

CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH

CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

CC [16] PTM: The soluble form is produced from the membrane form by

CC proteolytic processing.

CC [17] DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant

CC familial hibernian fever (FHF), a disease characterized by

CC recurrent fever, abdominal pain, localized tender skin lesions and

CC myalgia.

CC [18] SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC [19] SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC [20] DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".

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SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60468; AAA39751.1; -;
DR EMBL; M59377; AAA40464.1; -;
DR EMBL; X59238; CAA41922.1; -;
DR EMBL; X57796; CAA40936.1; -;
DR EMBL; L26349; AAA59361.1; -;
DR EMBL; M76656; AAA40465.1; -;
DR EMBL; M88067; AAA40465.1; JOINED.
DR EMBL; M76655; AAA40465.1; JOINED.
DR PIR; A38634; GQMST1.
DR PIR; S16677; S16677.
DR PIR; S19021; S19021.
DR HSP; P19438; IEXT.
DR MGD; MGI:131484; Tnftrsf1a.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death; 1.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 1A.
FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 213 235 POTENTIAL.
FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 356 441 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.

FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 195 BY SIMILARITY.
FT DISULFID 185 191 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 394 394 R -> G (IN REF. 6).
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 10.3%; Score 185; DB 1; Length 454;
Best Local Similarity 29.2%; Pred. No. 2.7e-07;
Matches 47; Conservative 20; Mismatches 84; Indels 10; Gaps 5;

QY 7 VLPVLVLAGSOLRVHTQGTNISESLKLRVRVHETDKKNCSEGLY---OGGPFCCQCPQPGK 63
Db 10 LLSLVLLALLMGIIHPSGVTLGLVPSGLDREK---RDSLCPQGVVHSHKNNISCTCTKCHKGT 66

QY 64 KVEDCKMNGTPTCAPCTEGKEYMDKNHVDKRCRRCTLCDEBHGLEVETNCTLTQNTKC 123
Db 67 YLVSDCPSGRDVTVCRECEKG-TFTASQNYLRQCLSKCTCKKEMSQVEISPCQADKDTVC 125

QY 124 KCKPDFYCDSPGCEH--CVRCASCEHGTLE-PCITATNTNC 161
Db 126 GKENQFQRYLSETHFQVDCSPCFNGTVPCKEYQNTVC 166

Search completed: May 9, 2003, 17:05:45
Job time : 17.3127 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:57:39 ; Search time 55.6647 Seconds
(without alignments)
801.926 Million cell updates/sec

Title: US-09-446-634A-22
Perfect score: 1804
Sequence: 1 MLGIWTLPLVLTSLSS.....KDTSDSENSFRNEIQSLV 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:.*
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10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:.*
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12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:.*
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18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1804	100.0	335	13 AAR28084	Human cell surface
2	1804	100.0	335	16 AAR78606	Human Fas protein.
3	1804	100.0	335	17 AAR9681	Human Fas antigen.
4	1804	100.0	335	17 AAR92528	hFas from plasmid
5	1804	100.0	335	18 AAW50289	Human Fas antigen.
6	1804	100.0	335	19 AAW49104	Fas protein. Mamm
7	1804	100.0	335	21 AAB19341	Amino acid encodin
8	1804	100.0	335	21 AAB01335	CD-95 (FAS/APO-1)
9	1804	100.0	335	22 AAB50517	Human tumour necro
10	1804	100.0	669	19 AAW64484	Human TNFR1 protei

11	1792	99.3	335	21	AAB36267	Human Fas receptor
12	1743	96.6	331	22	AAB50893	Human Fas receptor
13	1667.5	92.4	314	16	AAR76238	Fas-delta-TM. Hom
14	1667.5	92.4	314	17	AAR9682	Human Fas soluble
15	1655.5	91.8	314	20	AAW98070	Soluble Fas recept
16	1484	82.3	281	21	AAB26982	Human Fas. Homo s
17	1225	67.9	219	22	AAB66978	Fas protein. Unid
18	997	55.3	237	21	AAB53420	Human colon cancer
19	972	53.9	173	21	AAB36229	Human Fas receptor
20	966	53.5	600	16	AAR78610	Expression vector
21	956	53.0	600	17	AAR92526	Fas antigen #1. S
22	870.5	48.3	927	22	AAV97653	Flk-1extrafasTm/cy
23	857.5	47.5	436	21	AAV91026	Apoptobody3sc fusi
24	856	47.5	327	14	AAR41688	Murine Fas. Mus m
25	856	47.5	327	16	AAR78611	Murine Fas antigen
26	856	47.5	327	17	AAR92530	mFas sequence. Sy
27	856	47.5	327	21	AAB19344	Amino acid sequenc
28	852	47.2	327	20	AAW86241	Fas ligand (FasL)
29	852	47.2	920	22	AAV97652	Flt-1extrafasTm/cy
30	811.5	45.0	144	18	AAW50286	Human Fas antigen
31	811.5	45.0	159	18	AAW50288	Human Fas antigen
32	811.5	45.0	376	18	AAW50287	Antigenic peptide
33	811.5	45.0	376	19	AAW60037	CD44hextrafasTm/cy
34	806.5	44.7	431	22	AAV97650	CD44hextra/tmFasCy
35	751	41.6	436	22	AAV97651	Human Fas soluble
36	621.5	34.5	149	17	AAR99683	Human Fas soluble
37	599	32.6	121	23	ABR81752	Tumour necrosis fa
38	557	30.9	111	23	ABR81750	Tumour necrosis fa
39	535.5	29.7	170	21	AAB36228	Expression vector
40	534.5	29.6	576	16	AAR78613	Plasmid fragment p
41	530	29.4	169	16	AAR78612	Fas antigen #2. S
42	526.5	29.2	592	17	AAR92527	Fas/Apo-1/CD95 Dea
43	427	23.7	84	22	AAV97654	Fas-R protein frag
44	425	23.6	84	19	AAW62178	Human Fas/apoi pro
45	352	19.5	68	20	AAW93611	

ALIGNMENTS

RESULT 1
AAR28084
ID AAR28084 standard; Protein; 335 AA.
AC AC
AAR28084;
DT 12-MAR-1993 (first entry)
XX Human cell surface antigen.
DE Fas antigen; apoptosis; pF58; NGFR/TNFR family.
KW Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..16
FT /label= signal
FT Protein 17..335
FT /label= Fas_antigen
FT Modified-site 118..120
FT /label= N-glycosylation_site
FT /note= "putative"
FT Modified-site 136..138
FT /label= N-glycosylation_site
FT /note= "putative"
FT Domain 174..190
FT /label= transmembrane
FT Domain 17..173
FT /label= extracellular
FT /note= "cysteine-rich"
FT Domain 191..335
FT /label= cytoplasmic
XX

PN EP510691-A.
 XX 28-OCT-1992.
 XX 24-APR-1992; 92EP-0107060.
 XX 26-APR-1991; 91JP-0125234.
 XX (OSAB-) OSAKA BIOSCIENCE INST.
 XX Itoh N, Nagata S, Yonehara S;
 PI WPI; 1992-358914/44.
 DR N-PSDB; AAQ29959.
 XX
 XX DNA encoding human cell surface antigen - used to clarify
 PT apoptosis mechanism of various types of cell, and to prepare
 PT monoclonal antibodies that react with tumour cells expressing Fas
 XX
 PS Claim 3; Fig 1 and 2; 27pp; English.
 XX
 CC The Fas antigen is implicated in apoptosis. A cDNA clone encoding
 CC the antigen was isolated (pf58) and the amino acid sequence of Fas
 CC was deduced from it. The mature protein has a calculated mol.wt. of
 CC 36,000 and is a member of the NGFR/TNFR family of cell-surface
 CC membrane proteins. The inventors claim a protein comprising at
 CC least the extracellular domain of Fas antigen.
 XX
 SQ Sequence 335 AA;
 Query Match 100.0%; Score 1804; DB 13; Length 335;
 Best Local Similarity 100.0%; Pred. No. 2.4e-151;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 QY 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
 DB 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
 QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 DB 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 QY 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAIINLSDVLSKYITTTIAGVM 240
 DB 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAIINLSDVLSKYITTTIAGVM 240
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGCKEAYDTLIKDLKK 300
 DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGCKEAYDTLIKDLKK 300
 QY 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 DB 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 RESULT 2
 ID AAR78606
 XX AAR78606 standard; Protein; 335 AA.
 AC AAR78606;
 XX
 DT 19-FEB-1996 (first entry)
 XX
 DE Human Fas protein.
 XX
 XX Plasmid pf58; human Fas cDNA; soluble membrane protein;
 KW antibody production; diseases; treatment; prevention.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..16
 FT /label= sig_peptide
 FT Peptide 17..335
 FT /label= mat_peptide
 XX JP07115988-A.
 XX 09-MAY-1995.
 XX 26-OCT-1993; 93JP-0267644.
 XX 26-OCT-1993; 93JP-0267644.
 XX (NISR) JAPAN TOBACCO INC.
 XX WPI; 1995-202847/27.
 XX N-PSDB; AAQ95297.
 DR
 XX Preparation of soluble membrane proteins - for their use in antibody
 PT production for the treatment and prevention of related diseases
 XX
 PS Example 1; Pages 15-17; 51pp; Japanese.
 XX
 CC AAR78606 (human Fas protein) is encoded by the plasmid pf58 which
 CC contains hFas cDNA. The plasmid was used in the construction of an
 CC expression vector for the prodn. of recombinant soluble membrane
 CC proteins. The proteins can be used in antibody prodn. for the
 CC treatment and prevention of related diseases.
 XX
 SQ Sequence 335 AA;
 Query Match 100.0%; Score 1804; DB 16; Length 335;
 Best Local Similarity 100.0%; Pred. No. 2.4e-151;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 QY 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
 DB 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
 QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 DB 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 QY 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAIINLSDVLSKYITTTIAGVM 240
 DB 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAIINLSDVLSKYITTTIAGVM 240
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGCKEAYDTLIKDLKK 300
 DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGCKEAYDTLIKDLKK 300
 QY 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 DB 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 RESULT 3
 ID AAR99681
 XX AAR99681 standard; Protein; 335 AA.
 AC AAR99681;
 XX
 DT 10-OCT-1996 (first entry)
 XX Human Fas antigen.
 DE
 XX Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
 KW

KW angioimmunoblastic lymphadenopathy; AILD.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..16
FT /label= Sig_peptide
FT Protein 17..335
FT /label= Mat_protein
FT Domain 17..173
FT /label= Extracellular_domain
FT Domain 174..190
FT /label= Transmembrane_domain
FT Domain 191..335
FT /label= Cytoplasmic_tail
XX
PN W09620206-A1.
XX
XX 04-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US17083.
XX
XX 23-DEC-1994; 94US-0371263.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Cheng J, Liu C, Mountz JD, Zhou T;
PI WPI; 1996-321796/32.
DR N-PSDB; AAT34526.
XX
XX Natural, soluble form of Fas antigen secreted by human cells is
PT result of alternative mRNA processing - used to diagnose
PT Fas-associated disease, e.g. systemic lupus erythematosus
XX
PS Disclosure; Page 109-111; 152pp; English.
XX
XX A CDNA clone (AAT34526) codes for a membrane receptor-like protein,
CC Fas antigen (AAR99681). It was isolated from cDNA derived from the
CC peripheral blood mononuclear cells of systemic lupus erythematosus
CC (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients. 4
CC Soluble variants (AAR99682-85) were identified of the Fas antigen.
CC These arose by alternative splicing of Fas gene transcripts. The
CC Fas variants were present at higher levels in SLE and AILD patients
CC than the non-soluble Fas antigen.
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 17; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120
QY 121 RPTNTKCRCKPFFCNSTVCEHCDPCTKCEHGIIEKCTLTSTNTCKEGRSRLNGLWLCIL 180
DB 121 RPTNTKCRCKPFFCNSTVCEHCDPCTKCEHGIIEKCTLTSTNTCKEGRSRLNGLWLCIL 180
QY 181 LLPILPIVWKKKEVQKTCRKIRKENQGSHPSTLNPTVAINLSVDLSKYITTAGVM 240
DB 181 LLPILPIVWKKKEVQKTCRKIRKENQGSHPSTLNPTVAINLSVDLSKYITTAGVM 240
QY 241 TLSQVKGFFVRKNGVNEAKIDEIKNDNVQDTAEQKQVOLLRNWHQHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFFVRKNGVNEAKIDEIKNDNVQDTAEQKQVOLLRNWHQHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAERKIQTIIILKDTSDSENSFRNEIQSLV 335

DB 301 ANLCTLAERKIQTIIILKDTSDSENSFRNEIQSLV 335
RESULT 4
AAR92528
ID AAR92528 standard; Protein; 335 AA.
XX
XX AAR92528;
AC AAR92528;
XX
XX 06-SEP-1996 (first entry)
XX hFas from plasmid pCEV4/hFas.
DE
XX
XX Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW rheumatoid arthritis; serum; systemic lupus erythematosus.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX 1..16
FT Peptide /note= "hFas signal peptide"
FT Protein 17..335
FT /note= "mature hFas"
XX
XX W09601277-A1.
XX
XX 18-JAN-1996.
PD
XX
XX 03-MAR-1995; 95WO-JP00349.
XX
XX 14-FEB-1995; 95JP-0025637.
PR 06-JUL-1994; 94JP-0154706.
XX
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA (NISB) JAPAN TOBACCO INC.
XX
XX Hachiya T, Noguchi J, Yonehara S;
XX WPI; 1996-087635/09.
DR N-PSDB; AAT16303.
XX
XX Immunoassay method for soluble Fas antigen in body fluids - for
PT diagnosis of auto-immune diseases such as rheumatoid arthritis and
PT systemic lupus erythematosus
XX
XX Example 8; Page 49-52; 124pp; Japanese.
PS
XX
XX This sequence represents the sequence for the human Fas antigen contained
CC within the Plasmid pCEV4/hFas. The soluble Fas antigen is included in
CC the immunoassay kit of the invention. The kit is for the assay of
CC soluble Fas antigen and contains an immobilised anti-soluble Fas
CC monoclonal antibody, as well as the standard soluble Fas antigen
CC represented by this sequence. The assay is simple and has high accuracy,
CC high sensitivity, and is capable of assaying a number of different
CC specimens at the same time. The immunoassay is used on biological
CC samples (such as serum) and is useful for diagnosis of autoimmune
CC diseases such as rheumatoid arthritis or systemic lupus erythematosus
CC (SLE).
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 17; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120

QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIIVWVKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
DB 181 LLPIPLIIVWVKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335

RESULT 5
AAW50289
ID AAW50289 standard; Protein; 335 AA.
XX
AC AAW50289;
XX
DT 16-JUL-1998 (first entry)
XX
DE Human Fas antigen.
XX
KW Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
KW apoptosis modulation.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..16
FT Peptide /label= sig_peptide
FT Peptide 17..335
FT Peptide /label= mat_peptide
FT Region 17..173
FT /note= "claimed fragment"
XX
PN WO9742319-A1.
XX
PD 13-NOV-1997.
XX
PF 01-MAY-1997; 97WO-JP01502.
XX
PR 02-MAY-1996; 96JP-0135760.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
XX (OSAB-) OSAKA BIOSCIENCE INST.
XX
PI Nagata S, Nakamura N;
XX
XX WPI; 1997-558981/51.
XX N-PSDB; AAV07002.
XX
PT Fas antigen derivative containing modified extracellular region -
PT has low antigenicity, promotes apoptosis and is useful in treatment
PT of viral and other diseases
XX
PS Claim 2; Fig 1-2; 102pp; Japanese.
XX
CC The present sequence was used in the development of novel Fas
CC antigen derivatives, which contain a Fas antigen extracellular
CC region lacking one or more amino acid residues in the region from
CC the amino-terminal to (but excluding) the 1st cysteine residue
CC (preferably at least 29 residues are deleted).
CC The derivatives are effective regulators of apoptosis and can be
CC used (either by administration of the polypeptide, or by the use
CC of the coding DNA in gene therapy) to treat a range of diseases,
CC e.g. diabetes, arthritis, lupus and in particular viral diseases

CC such as hepatitis, influenza and HIV, by modulating apoptosis of
CC virus-infected cells.
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 18; Length 335;
Best local similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLWTLLPLVLTSVARLSSKSVNAQVTDINSKGLERKKTVTTVETONLEGLHHDGOFCH 60
DB 1 MGLWTLLPLVLTSVARLSSKSVNAQVTDINSKGLERKKTVTTVETONLEGLHHDGOFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDEGHLEVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDEGHLEVEINCT 120
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIIVWVKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
DB 181 LLPIPLIIVWVKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335

RESULT 6
AAW49104
ID AAW49104 standard; Protein; 335 AA.
XX
AC AAW49104;
XX
DT 18-NOV-1998 (first entry)
XX
DE Fas protein.
XX
KW Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
KW prophylactic; AIDS.
XX
OS Mammalia sp.
XX

FH Key Location/Qualifiers
FT Peptide 1..16
FT Peptide /note= "Signal peptide"
FT Protein 17..335
FT Protein /note= "Fas protein"
FT Region 17..172
FT /note= "The portion of a Fas protein which can be
FT fused to a Fc polypeptide to form a Fas-Fc
FT fusion protein"
XX
PN WO9835692-A1.
XX
PD 20-AUG-1998.
XX
PF 17-FEB-1998; 98WO-GB00485.
XX
PR 17-FEB-1997; 97GB-0003276.
XX (ISIS-) ISIS INNOVATION LTD.
XX
PI Screamon GR, Xu X;
XX

DR WPI; 1998-456867/39.
XX N-PSDB; AAV32993.
PT Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
PT diseases - by interfering with interaction of Fas with Fas-ligand
PT expressed on activated CD4+ cells, e.g. cells infected with HIV
XX
PS Disclosure; Fig 7; 71pp; English.
XX
XX The present sequence represents a Fas protein sequence used in the
CC method of the invention. The method is concerned with reducing
CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
CC cells in an immune cell population which also comprises of Fas-ligand
CC (FasL)-expressing activated CD4+ cells. It involves contacting this
CC immune cell population with an effective amount of an agent (e.g. a
CC soluble Fas-FC fusion protein) which would interfere with the
CC interaction between Fas and FasL. Therefore, the method is useful for
CC identifying suitable agents which can reduce depletion of activated
CC Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
CC is the use of the agent in the manufacture of therapeutic compositions.
CC Apoptosis of lymphocytes can be triggered by the interaction of the
CC cell surface receptor Fas and its ligand FasL. By interfering with
CC this interaction, the method described and its preparations can prevent
CC apoptosis of CD8+ TK lymphocytes caused by expression of FasL on
CC activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
CC especially the result of CD4+ cell infection with an immunodeficiency
CC virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
CC virus (SIV). The claimed prevention of apoptosis may then allow
CC maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
CC towards the CD4+ cells infected with the infectious agent, enabling
CC treatment (prophylactic and/or therapeutic) of immunodeficiency
CC diseases e.g. AIDS.
XX
XX Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 19; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
Qy 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Qy 181 LLPIPLIVVVRKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIVVVRKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIQITILKDTSDSENSNFRNEIQSLV 335
Db 301 ANLCTLAEKIQITILKDTSDSENSNFRNEIQSLV 335
RESULT 7
AAB19341
ID AAB19341 standard; Protein; 335 AA.
XX
AC AAB19341;
XX
DT 06-MAR-2001 (first entry)
XX
DE Amino acid encoding a human Fas (Apo-1) protein.

XX Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;
KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
KW autoimmune disease; inflammatory disease; lymphoma.
XX Homo sapiens.
XX OS
XX WO2000061150-A1.
XX
XX 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US09540.
XX
XX 12-APR-1999; 99US-0290640.
XX (ISIS-) ISIS PHARM INC.
XX Dean NM, Marcusson EG;
XX WPI; 2000-628395/60.
XX N-PSDB; AAC61798.
XX Antisense oligonucleotides for treating hepatitis and colon, liver or
PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
PT 1 (Fap-1) expression
XX
XX Example 2; Page 73-74; 116pp; English.
XX
XX The present sequence represents human Fas (Apo-1). The specification
CC describes antisense compounds which are targeted to the 5'-untranslated
CC region, translational start site, translational termination region
CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
CC ligand (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine
CC phosphatase). The antisense compounds are used to inhibit the
CC expression of Fas, FasL or Fap-1 in cells or tissues. They are used
CC to treat autoimmune or inflammatory diseases such as hepatitis. They
CC can also be used to treat cancer, especially colon, liver or lung
CC cancer or lymphoma.
XX
XX Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 21; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
Qy 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Qy 181 LLPIPLIVVVRKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIVVVRKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIQITILKDTSDSENSNFRNEIQSLV 335
Db 301 ANLCTLAEKIQITILKDTSDSENSNFRNEIQSLV 335
RESULT 8
AAB01335
ID AAB01335 standard; Protein; 335 AA.

XX AAB01335;
AC
XX
DT 25-SEP-2000 (first entry).
XX
DE CD-95 (FAS/APO-1) death receptor.
XX
KW UL144; death receptor; apoptosis; programmed cell death; FAS;
KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW human.
XX
XX Homo sapiens.
OS
XX
XX WO200034335-A2.
PN
XX
XX 15-JUN-2000.
XX
XX 03-DEC-1999; 99WO-US26035.
PF
XX 04-DEC-1998; 98US-0205018.
PR
XX (SCHE) SCHERING CORP.
PA
XX
XX Leong C, Phillips JH;
PI
XX
XX WPI; 2000-423383/36.
DR
XX
XX Purified or recombinant polypeptide for modulating apoptosis comprises
PT a sequence which binds to an antibody specific for UL144 or its
PT fragments
PT
XX
XX Disclosure; Page 64-65; 76pp; English.
PS
XX
XX A pure or recombinant polypeptide which binds to a polyclonal antibody
CC specific for the mature UL144 is useful for screening molecules which
CC block induction of apoptosis or interfere with antiapoptotic activity.
CC The polypeptide is also useful for modulating apoptosis and useful in
CC treatment of conditions associated with abnormal physiology or
CC development, such as cancer or degenerative conditions and for
CC regulation of viral infection and replication. At least five
CC different death receptors are known, which include the CD95
CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
XX
XX Sequence 335 AA;
SQ
Query Match 100.0%; Score 1804; DB 21; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 M LGIWTLLPLVLTSVARLSKSNVAQVTDINSGLELRKVTVTQNLGLHHDGQFCH 60
Dbb 1 M LGIWTLLPLVLTSVARLSKSNVAQVTDINSGLELRKVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHSSKRCRLCDEGHLEVEINCT 120
Dbb 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHSSKRCRLCDEGHLEVEINCT 120
QY 121 RTQNTKCRCKPNFCNTVCEHDCPCTKCEHGIKECTLFSNTKCKEGRSRLGWLCLL 180
Dbb 121 RTQNTKCRCKPNFCNTVCEHDCPCTKCEHGIKECTLFSNTKCKEGRSRLGWLCLL 180
QY 181 LLPLPLVWVRKKEVQTKRHRKENGSGHESPTLPETVAINLSVDVLSKYITTAGVM 240
Dbb 181 LLPLPLVWVRKKEVQTKRHRKENGSGHESPTLPETVAINLSVDVLSKYITTAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEINDNVQDTAEQKVOLLRNHWHQHGKKEAYDTLLKDLKK 300
Dbb 241 TLSQVGFVRKNGVNEAKIDEINDNVQDTAEQKVOLLRNHWHQHGKKEAYDTLLKDLKK 300
QY 301 ANCLTAEKIQTIILKIDITSSENSNFRNEIOSLV 335
|||||

Db 301 ANCLTAEKIQTIILKIDITSSENSNFRNEIOSLV 335
RESULT 9
AAB50517
ID AAB50517 standard; Protein; 335 AA.
XX
AC AAB50517;
XX
DT 15-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor FAS protein SEQ ID NO:7.
XX
KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
OS Homo sapiens.
XX
XX WO2000071150-A1.
PN
XX
XX 30-NOV-2000.
PD
XX
XX 18-MAY-2000; 2000WO-US13515.
PF
XX
XX 20-MAY-1999; 99US-0135164.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Wei Y, Ruben SM, Gentz RL, Ni J;
PI
XX
XX WPI; 2001-041051/05.
DR
XX
XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection -
PT
XX Disclosure; Fig 2; 285pp; English.
PS
XX
CC The present invention describes the human TRID protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities and can be used in gene therapy. The TRID polynucleotides
CC are useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis-factor receptor used in
CC comparison with TRID in the exemplification of the present invention.
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 22; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIWTLPLVLTTSVARLSKSVNAQVTDINSKGLRLKTKTTTETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTTSVARLSKSVNAQVTDINSKGLRLKTKTTTETQNLGLHHDGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDEGHGVEINCT 120
Qy 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKEGRSRLGLWLCLL 180
Db 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKEGRSRLGLWLCLL 180
Qy 181 LLPIPLIIVWVRKEVQKTCRKRKRNQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIIVWVRKEVQKTCRKRKRNQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335

RESULT 10

AAW64484
ID AAW64484 standard; Protein; 569 AA.

AC AAW64484;

XX 20-OCT-1998 (first entry)

XX Human TNFR1 protein.

XX Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation;
KW agonist; tumour necrosis factor; TNF; ligand; autoimmune disease;
KW infection; graft rejection; antagonist; inhibitor; diagnostic.

XX Homo sapiens.

XX WO9832856-A1.

XX 30-JUL-1998.

XX 27-JAN-1998; 98WO-US01464.

XX 05-FEB-1997; 97US-0037829.

XX 28-JAN-1997; 97US-0035722.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

XX Dixit VM, Gentz RL, Ni J, Pan JG, Rosen CA;

XX WPI; 1998-427952/36.

XX Nucleic acid encoding human death domain-containing receptor 4 -
PT useful for therapeutic modulation of apoptosis, in e.g. cancer and
PT autoimmune diseases

XX Disclosure; Fig 2; 92pp; English.

XX This sequence represents a human tumour necrosis factor receptor-1 which
CC is used in a method resulting in the isolation of a human death domain
CC containing receptor 4, DR4. DR4 agonists are used to increase apoptosis
CC induced by tumour necrosis factor (TNF)-family ligands, e.g. in cases of
CC cancer, autoimmune disease, viral or other infections, inflammation,
CC graft vs. host disease, acute or chronic graft rejection. Antagonists of
CC DR4 are used to inhibit such apoptosis, e.g. in cases of acquired immune
CC deficiency syndrome, neurodegenerative disease, myelodysplastic syndrome,
CC ischaemic injury, toxin-induced liver damage, septic shock, cachexia and
CC anorexia, also a wide range of inflammatory conditions. DR4 of fragments

CC of the protein are used diagnostically, e.g. to detect mutant forms of
CC DR4 (possibly associated with disease), for isolating the DR4 gene or
CC related sequences and for chromosomal mapping.

XX Sequence 669 AA;

Qy Query Match 100.0%; Score 1804; DB 19; Length 669;
Db Best Local Similarity 100.0%; Pred. No. 6.1e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIWTLPLVLTTSVARLSKSVNAQVTDINSKGLRLKTKTTTETQNLGLHHDGQFCH 60

Db 1 MGIWTLPLVLTTSVARLSKSVNAQVTDINSKGLRLKTKTTTETQNLGLHHDGQFCH 60

Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDEGHGVEINCT 120

Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDEGHGVEINCT 120

Qy 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKEGRSRLGLWLCLL 180

Db 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKEGRSRLGLWLCLL 180

Qy 181 LLPIPLIIVWVRKEVQKTCRKRKRNQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240

Db 181 LLPIPLIIVWVRKEVQKTCRKRKRNQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240

Qy 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300

Db 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300

Qy 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335

Db 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335

RESULT 11

AAAB36267
ID AAB36267 standard; Protein; 335 AA.

XX AAB36267;

XX 20-FEB-2001 (first entry)

XX Human Fas receptor.

XX Human; death domain containing receptor; DR3-VL; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis.

XX Homo sapiens.

XX WO200064465-A1.

XX 02-NOV-2000.

XX 21-APR-2000; 2000WO-US10741.

XX 22-APR-1999; 99US-0130488.

XX 28-MAY-1999; 99US-0136741.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

XX (YUGG/) YU G.

XX (NIJJ/) NI J.

XX (GENT/) GENTZ R L.

XX (DILL/) DILLON P J.

XX (DIXI/) DIXIT V M.

XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;

XX WPI; 2000-687263/67.

XX Treating graft-versus-host disease, cancer, immunodeficiency or an

PT autoimmune disease comprising administering an antibody to Death Domain
 PT Containing Receptor proteins and a second therapeutic agent -
 PS Disclosure; Fig 3; 273pp; English.

XX The present invention provides the protein and coding sequences for two
 CC death domain containing receptors, designated DR3 and DR3-VI. These
 CC receptors are involved in apoptosis, and the sequences given can be used
 CC in the treatment of cancers, infections, cardiovascular disorders such as
 CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
 CC and congenital heart defects, neurodegenerative diseases including
 CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
 CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
 CC and to promote angiogenesis and wound healing.

SQ Sequence 335 AA;

Query Match 99.3%; Score 1792; DB 21; Length 335;
 Best Local Similarity 99.7%; Pred. No. 2.8e-150;
 Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60

DB 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60

QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 120

DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 120

QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLGWLCLL 180

DB 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLGWLCLL 180

QY 181 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 240

DB 181 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 240

QY 241 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 300

DB 241 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 300

QY 301 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 335

DB 301 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 335

RESULT 12

AAB50893

XX ID AAB50893 standard; Protein; 331 AA.

XX AC AAB50893;

XX DT 19-MAR-2001 (first entry)

XX DE Human Fas receptor.

XX Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective;
 KW antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiant;
 KW vasotrophic; antiallergic; antidiabetic; vulnerary; ophthalmological;
 KW antiviral; antibacterial; antifungal; antiparasitic; gene therapy;
 KW tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder;
 KW apoptosis; cardiovascular disorder; inflammatory disease; wound;
 KW infection; neurological disease; Fas receptor; protein coordinate data.

XX OS Homo sapiens.

XX PN WO200073321-A1.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14554.

XX PR 28-MAY-1999; 99US-0136786.

PR 07-JUL-1999; 99US-0142563.
 PR 15-JUL-1999; 99US-0144023.
 XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ni J;

XX DR WPI; 2001-025250/03.

XX Nucleic acid encoding a tumor necrosis factor receptor 10, useful in
 PT the diagnosis, treatment or prevention of cancer, autoimmune disorders,
 PT and diseases and disorders associated with apoptosis -
 XX Disclosure; Fig 2; 212pp; English.

XX The present sequence is given in a specification relating to an isolated

CC nucleic acid encoding a human tumour necrosis factor receptor TR10.
 CC The TR10 polynucleotide, polypeptide, antibodies, agonists and
 CC antagonists are useful in the diagnosis, treatment or prevention of
 CC cancer, such as breast and ovarian cancer and leukaemia; autoimmune
 CC disorders such as multiple sclerosis, Crohn's disease and graft versus
 CC host disease; diseases associated with increased apoptosis such as AIDS,
 CC Alzheimer's disease and Parkinson's disease; cardiovascular disorders
 CC such as limb ischaemia and congenital heart defects; inflammatory
 CC diseases e.g. allergy; wound healing; disorders associated with
 CC neovascularisation, e.g. diabetic retinopathy; infectious diseases such
 CC as viral, bacterial, fungal and parasitic infections; and neurological
 CC diseases such as amyotrophic lateral sclerosis.

SQ Sequence 331 AA;

Query Match 96.6%; Score 1743; DB 22; Length 331;
 Best Local Similarity 98.8%; Pred. No. 6e-146;
 Matches 331; Conservative 0; Mismatches 4; Indels 4; Gaps 4;

QY 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60

DB 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60

QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 120

DB 60 -PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 118

QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLGWLCLL 180

DB 119 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLGWLCLL 177

QY 181 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 240

DB 178 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 237

QY 241 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 300

DB 238 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 297

QY 301 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 335

DB 298 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 331

RESULT 13

AAR76238

ID AAR76238 standard; Protein; 314 AA.

XX AC AAR76238;

XX DT 06-NOV-1995 (first entry)

XX DE Fas-delta-TM.

XX Fas-delta-TM; transmembrane deletion; apoptosis; antibody;

KW adoptive immunotherapy; transgenic animal.

XX

```
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..16
FT /label= Sig_peptide
FN WO9513701-A.
PD 26-MAY-1995.
PF 15-NOV-1994; 94WO-US13173.
PR 15-NOV-1993; 93US-0152443.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX Barr PJ, Kiefer MC, Shapiro JP;
XX WPI; 1995-200120/26.
DR N-PSDB; AAQ93879.
XX
XX New nucleic acid encoding Fas protein without its trans-membrane region
XX - and related vectors, transformed cells, transgenic animals, protein and
XX antibodies, useful for control of Fas mediated apoptosis
XX
XX Claim 9; Fig.3-1 to 3-4; 38pp; English.
XX
XX mRNA was obt'd. from human lymphocytes and PCR was used to make
XX cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
XX region) mRNA. The PCR product was ligated into phluescript and the
XX recombinant plasmid was used to transfect E. coli DHS-alpha cells. The
XX insert sequence of pBluescript-Fas-delta-TM encoded the protein
XX given in AAR76238.
XX
SQ Sequence 314 AA;

Query Match 92.4%; Score 1667.5; DB 16; Length 314;
Best Local Similarity 93.7%; Pred. No. 2.7e-139;
Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60

Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDGHGCLVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDGHGCLVEINCT 120

Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEGRSRLGLWLCIL 180
Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEE----- 168

Qy 181 LPLTPIVVRKEVQKTCRKHRENQSHSPETLNPTETVAINLSVDLSKYITTIAGVM 240
Db 169 -----VRRKEVQKTCRKHRENQSHSPETLNPTETVAINLSVDLSKYITTIAGVM 219

Qy 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHGKKEAYDTLLKDKK 300
Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHGKKEAYDTLLKDKK 279

Qy 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335
Db 280 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 314

RESULT 14
ID AAR99682
XX AAR99682 standard; Protein; 314 AA.
AC AAR99682;
XX
XX 10-OCT-1996 (first entry)
XX
```

```
DE Human Fas soluble antigen Fas dell.
XX
XX Fas antigen: autoimmune disease; systemic lupus erythematosus; SLE;
KW angioimmunoblastic lymphadenopathy; AILD.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..16
FT /label= Sig_peptide
FT Protein 17..314
FT /label= Mat_protein
FT /note= "soluble Fas dell antigen"
FT Domain 17..168
FT /label= Extracellular_domain
FT /note= "the 5 C-terminal residues of the
FT Fas antigen extracellular domain are
FT deleted in Fas dell"
FT Domain 169..314
FT /label= Cytoplasmic_domain
FT Peptide 164..173
FT /note= "preferred peptide from breakpoint region
FT (claim 4, page 132)"
FT Peptide 164..174
FT /note= "preferred peptide from breakpoint region"
FT Peptide 161..171
FT /note= "preferred peptide from breakpoint region"
XX
XX WO9620206-A1.
XX 04-JUL-1996.
XX 22-DEC-1995; 95WO-US17083.
XX 23-DEC-1994; 94US-0371263.
XX (UABR-) UAB RES FOUND.
XX Cheng J, Liu C, Mountz JD, Zhou T;
XX
XX WPI; 1996-321796/32.
DR N-PSDB; AAT34527.
XX
XX Natural, soluble form of Fas antigen secreted by human cells is
XX result of alternative mRNA processing - used to diagnose
XX Fas-associated disease, e.g. systemic lupus erythematosus
XX
XX Claim 4; Page 114-16; 152pp; English.
XX
XX A natural, soluble Fas antigen variant (AAR99682), designated Fas
XX dell, and other Fas variants (AAR99683-85) are derived by alternative
XX splicing of Fas gene transcripts. A cDNA clone (AAT34527) coding for
XX the variant was obt'd. from human peripheral blood mononuclear cells.
XX The Fas dell variant lacks the transmembrane domain of insoluble
XX Fas antigen (AAR99681). Recombinant dell variant, or fragments of
XX it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells.
XX Detection of increased levels of soluble forms of Fas antigen can
XX be used to diagnose autoimmune diseases, esp. systemic lupus
XX erythematosus and angioimmunoblastic lymphadenopathy.
XX
XX Sequence 314 AA;

Query Match 92.4%; Score 1667.5; DB 17; Length 314;
Best Local Similarity 93.7%; Pred. No. 2.7e-139;
Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60

Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDGHGCLVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDGHGCLVEINCT 120
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QY 121 RTONTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKEGRSRLNGLCLL 180
 Db 121 RTONTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKE----- 168
 QY 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPEVAINLSDVDLSKIYITTIAGVM 240
 Db 169 -----VKRKEVQKTCRKHKENOGSHESPTLNPEVAINLSDVDLSKIYITTIAGVM 219
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNWHQHGKKEAYDTLIKDLKK 300
 Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNWHQHGKKEAYDTLIKDLKK 279
 QY 301 ANLCTLAEKIQTILKDTSDSENSFRNEIOSLV 335
 Db 280 ANLCTLAEKIQTILKDTSDSENSFRNEIOSLV 314

RESULT 15
 AAW98070
 ID AAW98070 standard; Protein; 314 AA.
 XX
 AC AAW98070;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Soluble Fas receptor.
 XX
 KW Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;
 KW graft versus host disease; autoimmune disease; psoriasis;
 KW rheumatoid arthritis; systemic lupus erythematosus; gene therapy.
 XX
 OS Mammalia.

Key Location/Qualifiers
 FH Peptide 1..16
 FT /note= "signal peptide"
 FT Protein 17..314
 FT /note= "mature protein"
 FT Misc-difference 109
 FT /note= "encoded by GAA"
 FT Modified-site 118
 FT /note= "N-glycosylated"
 XX
 PN W09903999-A1.
 XX
 PD 28-JAN-1999.
 XX
 PF 16-JUL-1998; 98WO-US14771.
 XX
 PR 17-JUL-1997; 97US-0052829.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Chen J, Nabel GJ;
 XX
 DR WPI; 1999-132243/11.
 DR N-PSDB; AAX24878.
 XX
 PT Inhibition of proinflammatory responses - using an agent which
 PT modulates FasL stimulation, used for treating graft versus host
 PT disease or autoimmune disease
 XX
 PS Disclosure; Fig 4B; 7lpp; English.
 XX
 CC This present sequence is a soluble Fas receptor. The invention
 CC provides a method for inhibiting a proinflammatory response in a
 CC cell mixture by administering an immunosuppressive agent which
 CC inhibits the proinflammatory activity of Fas ligand (FasL). In some
 CC embodiments, an FasL is coadministered with the immunosuppressive
 CC agent, and the cell mixture comprises neutrophil cells. The method
 CC can be practised in vitro, ex vivo or in vivo. Suitable
 CC immunosuppressive agents include antisense molecules that inhibit

CC endogenous FasL expression, soluble Fas receptors or variants,
 CC ribozymes that inhibit the endogenous expression of FasL, drugs
 CC that inhibit FasL signalling, agents that induce the endogenous
 CC expression of transforming growth factor (TGF)-beta, and
 CC polynucleotides coding for an immunosuppressive agent such as
 CC TGF-beta. The method can be used for treating diseases associated
 CC with an undesired FasL-mediated proinflammatory response, e.g.
 CC graft versus host disease, or an autoimmune disease such as
 CC systemic lupus erythematosus, rheumatoid arthritis and psoriasis.
 CC The invention also provides a method for identifying agents which
 CC modulate FasL stimulation of a proinflammatory response.
 XX

SQ Sequence 314 AA;

Query Match 91.8%; Score 1655.5; DB 20; Length 314;
 Best Local Similarity 93.1%; Pred. No. 3.1e-138;
 Matches 312; Conservative 0; Mismatches 2; Indels 21; Gaps 1;

QY 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
 Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
 QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLCDGEGHLEVEINCT 120
 Db 61 KPCPPGERKARDCTCNGDEPCVPCQEGKEYTDKAHFSSKRCRCLCDGEGHLEVEINCT 120
 QY 121 RTONTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKEGRSRLNGLCLL 180
 Db 121 RTONTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKE----- 168
 QY 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPEVAINLSDVDLSKIYITTIAGVM 240
 Db 169 -----VKRKEVQKTCRKHKENOGSHESPTLNPEVAINLSDVDLSKIYITTIAGVM 219
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNWHQHGKKEAYDTLIKDLKK 300
 Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNWHQHGKKEAYDTLIKDLKK 279
 QY 301 ANLCTLAEKIQTILKDTSDSENSFRNEIOSLV 335
 Db 280 ANLCTLAEKIQTILKDTSDSENSFRNEIOSLV 314

Search completed: May 9, 2003, 17:05:04
 Job time : 57.6647 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:03:26 ; Search time 13.1571 Seconds
(without alignments)
749.153 Million cell updates/sec

Title: US-09-446-634A-22
Perfect score: 1804
Sequence: 1 MGIWTLPLVLTSVARLSS.....KDTSDSENSFRNFIQSLV 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/iaa/PCRTUS_COMB.pep.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	335	2 US-08-219-237B-2	Sequence 2, Appl
2	1804	100.0	335	2 US-08-409-338-1	Sequence 1, Appl
3	1804	100.0	335	4 US-09-290-640-2	Sequence 2, Appl
4	1804	100.0	335	4 US-09-006-353A-7	Sequence 7, Appl
5	1804	100.0	335	4 US-08-468-560C-2	Sequence 2, Appl
6	1804	100.0	335	4 US-09-180-100-20	Sequence 20, Appl
7	1804	100.0	335	4 US-09-565-918-3	Sequence 3, Appl
8	1804	100.0	335	4 US-09-573-986-7	Sequence 7, Appl
9	1804	100.0	335	5 PCT-US95-17083-2	Sequence 2, Appl
10	1804	100.0	669	4 US-09-013-895A-3	Sequence 3, Appl
11	1804	100.0	669	4 US-09-448-868-3	Sequence 3, Appl
12	1792	99.3	335	4 US-08-815-469-6	Sequence 6, Appl
13	1743	96.6	331	4 US-09-086-483A-3	Sequence 3, Appl
14	1667.5	92.4	314	1 US-08-444-231-19	Sequence 19, Appl
15	1667.5	92.4	314	1 US-08-152-443A-19	Sequence 19, Appl
16	1667.5	92.4	314	5 PCT-US95-17083-4	Sequence 4, Appl
17	1484	82.3	281	4 US-09-527-236A-3	Sequence 3, Appl
18	1225	67.9	219	3 US-08-974-022-45	Sequence 45, Appl
19	1225	67.9	219	4 US-08-795-445A-45	Sequence 45, Appl
20	1225	67.9	219	4 US-08-795-447A-45	Sequence 45, Appl
21	1225	67.9	219	4 US-08-974-186-45	Sequence 45, Appl
22	1225	67.9	219	4 US-08-795-446B-45	Sequence 45, Appl
23	1225	67.9	219	4 US-08-706-945D-131	Sequence 131, App
24	942	52.2	167	4 US-08-828-683A-22	Sequence 22, Appl
25	893	49.5	157	4 US-09-180-100-15	Sequence 15, Appl
26	856	47.5	327	4 US-09-290-640-66	Sequence 66, Appl
27	811.5	45.0	144	4 US-09-180-100-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-08-219-237B-2
; Sequence 2, Application US/08219237B

; Patent No. 5874546

; GENERAL INFORMATION:

; APPLICANT: NAGATA, Shigekazu

; APPLICANT: ITOH, Naoto

; APPLICANT: YONEHARA, Shin

; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James W. Hellwege

; STREET: P.O. Box 2266 Eads Station

; CITY: Arlington

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/219,237B

; FILING DATE: 28-MAR-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/872,129

; FILING DATE: 22-APR-1992

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: James W. Hellwege

; REGISTRATION NUMBER: 28,808

; REFERENCE/DOCKET NUMBER: 516762

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 335 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-219-237B-2

Query Match 100.0%; Score 1804; DB 2; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.6e-160;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60

|||||

Db 1 MGIWTLPLVLTSVARLSSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60

|||||

QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDRGHGLEVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDRGHGLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHLIKECTLTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHLIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKHKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKHKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIOTIILKDIITSDSENSFRNEIQSLV 335
Db 301 ANLCTLAEKIOTIILKDIITSDSENSFRNEIQSLV 335

RESULT 2

US-08-409-338-1

; Sequence 1, Application US/08409338

; Patent No. 5891434

; GENERAL INFORMATION:

; APPLICANT: Kramer, Peter H.

; APPLICANT: Debatin, Klaus-Michael

; APPLICANT: Trauth, Bernhard C.

; APPLICANT: Behrmann, Iris

; APPLICANT: Dhein, Jens

; APPLICANT: Klas, Christiane

; APPLICANT: M ller, Peter

; APPLICANT: Falk, Werner

; APPLICANT: Oehm Alexander

; APPLICANT: Daniel, Peter T.

; TITLE OF INVENTION: Monoclonal Antibodies to the Apo-1 Antigen

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington, MA 02173

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/409,338

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,644

; FILING DATE: 16-JUN-1994

; APPLICATION NUMBER: US 07/691,016

; FILING DATE: 17-JUN-1991

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Brook, David E.

; REGISTRATION NUMBER: 22,592

; REFERENCE/DOCKET NUMBER: CTR89-35A2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 335 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-409-338-1

Query Match 100.0%; Score 1804; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDRGHGLEVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDRGHGLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHLIKECTLTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHLIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKHKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKHKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIOTIILKDIITSDSENSFRNEIQSLV 335
Db 301 ANLCTLAEKIOTIILKDIITSDSENSFRNEIQSLV 335

RESULT 3

US-09-290-640-2

; Sequence 2, Application US/09290640

; Patent No. 6204055

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Marcussan, Eric G.

; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

; FILE REFERENCE: ISPH-0351

; CURRENT APPLICATION NUMBER: US/09/290,640

; CURRENT FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 335

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-290-640-2

Query Match 100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDRGHGLEVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDRGHGLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHLIKECTLTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHLIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKHKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKHKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300

Qy 301 ANLCTLAETIILKIDITSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIILKIDITSDSENSFRNEIQSLV 335

RESULT 4
US-09-006-353A-7
; Sequence 7, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-006-353A-7

Query Match 100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTVETONLEGLHHGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTVETONLEGLHHGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHGLEVEINCT 120
Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
Qy 181 LLPIPLIYVWKRKEVQKTCRKHKRKNQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKHKRKNQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAETIILKIDITSDSENSFRNEIQSLV 335

Db 301 ANLCTLAETIILKIDITSDSENSFRNEIQSLV 335
RESULT 5
US-08-468-560C-2
; Sequence 2, Application US/08468560C
; Patent No. 6270998
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,560C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR., GERLAD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 20-4393P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-560C-2

Query Match 100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTVETONLEGLHHGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTVETONLEGLHHGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHGLEVEINCT 120
Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
Qy 181 LLPIPLIYVWKRKEVQKTCRKHKRKNQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKHKRKNQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAETIILKIDITSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIILKIDITSDSENSFRNEIQSLV 335

```
RESULT 6
US-09-180-100-20
; Sequence 20, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-20

Query Match      100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGLWCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGLWCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335

RESULT 7
US-09-565-918-3
; Sequence 3, Application US/09565918.
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722

Query Match      100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGLWCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGLWCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335

RESULT 8
US-09-573-986-7
; Sequence 7, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-7

Query Match      100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGLWCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGLWCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
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Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
QY 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
Db 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335

RESULT 9
PCT-US95-17083-2
; Sequence 2, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17083-2

Query Match 100.0%; Score 1804; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
QY 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
Db 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335

RESULT 10
US-09-013-895A-3
; Sequence 3, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.

; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,895A
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-013-895A-3

Query Match 100.0%; Score 1804; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 4.1e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
QY 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
Db 181 LLPIPLIIVWKRKEVQKTCRKHKENOGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335

RESULT 11
US-09-448-868-3
; Sequence 3, Application US/09448868
; Patent No. 6461923
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian

APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-868-3

Query Match 100.0%; Score 1804; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 4.1e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSKSNVAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSNVAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLSNTKKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLSNTKKEGSRNLGWLCLL 180
QY 181 LLPIPLVWVKRKEVQKTCRKHKENQSGHESPTLNPETVAINLSVDLSKYITTAGVM 240
Db 181 LLPIPLVWVKRKEVQKTCRKHKENQSGHESPTLNPETVAINLSVDLSKYITTAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHLHGKKEAYDFLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHLHGKKEAYDFLIKDLKK 300
QY 301 ANLCTIAEQITLILKIDTSSENSFRNEIQSLV 335
Db 301 ANLCTIAEQITLILKIDTSSENSFRNEIQSLV 335

RESULT 12
US-08-815-469-6
Sequence 6, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-815-469-6

Query Match 99.3%; Score 1792; DB 4; Length 335;
Best Local Similarity 99.7%; Pred. No. 2.1e-159;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSKSNVAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSNVAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLSNTKKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLSNTKKEGSRNLGWLCLL 180
QY 181 LLPIPLVWVKRKEVQKTCRKHKENQSGHESPTLNPETVAINLSVDLSKYITTAGVM 240
Db 181 LLPIPLVWVKRKEVQKTCRKHKENQSGHESPTLNPETVAINLSVDLSKYITTAGVM 240

Qy 241 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNNHQLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIOTIILKIDTSDSENSFNREIQLSLV 335
Db 301 ANLCTLAEKIOTIILKIDTSDSENSFNREIQLSLV 335

RESULT 13

US-09-086-483A-3
; Sequence 3, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-483A-3

Query Match 96.68; Score 1743; DB 4; Length 331;
Best Local Similarity 98.88; Pred. No. 7.6e-155;
Matches 331; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
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Db 60 -PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGLEYEINCT 118
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Db 178 LLPIPLIIVWVRKEVQKTCRKHRENQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 237
Qy 241 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNNHQLHGKKEAYDTLIKDLKK 300
Db 238 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVLRLNNHQLHGKKEAYDTLIKDLKK 297
Qy 301 ANLCTLAEKIOTIILKIDTSDSENSFNREIQLSLV 335
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RESULT 14

US-08-444-231-19
; Sequence 19, Application US/08444231
; Patent No. 5652210
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,231
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/152,443
; FILING DATE: 15-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-444-231-19

Query Match 92.48; Score 1667.5; DB 1; Length 314;
Best Local Similarity 93.78; Pred. No. 8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
Qy 1 MGLIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVETQNLGLHHDGQFCH 60
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Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDTLIKDLKK 279
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RESULT 15

US-08-152-443A-19
; Sequence 19, Application US/08152443A
; Patent No. 5663070
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,443A
; FILING DATE: 15-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-152-443A-19

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Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVETQNLGLHHDGFCH 60
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QY 181 LLPIPLIVWVKRKEVQKTCRKHRENQGSHPSTLNPEVAINLSDVDLSKYITTIAGVM 240
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Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDTLIKDLKK 279
QY 301 ANLCTLAEKIQTIIILKDITSDSENSFNFRNEIOSLV 335
Db 280 ANLCTLAEKIQTIIILKDITSDSENSFNFRNEIOSLV 314

Search completed: May 9, 2003, 17:08:24
Job time : 15.1571 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:05:23 ; Search time 16.6994 Seconds
(without alignments)
1846.092 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804

Sequence: 1 MGIWTLPLVLTSLVARLSS.....KDTSDSENFRNIQISLV 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1804	100.0	335	10	US-09-826-212-7
2	1804	100.0	335	10	US-09-802-669-2
3	1804	100.0	335	10	US-09-949-713-20
4	1804	100.0	335	10	US-09-874-138-4
5	1804	100.0	335	10	US-09-884-987-2
6	1804	100.0	335	10	US-09-935-727-9
7	1804	100.0	335	12	US-10-005-842-4
8	1804	100.0	669	9	US-10-226-296-3
9	1804	100.0	669	9	US-10-226-318-3
10	1792	99.3	335	9	US-09-314-889-6
11	1792	99.3	335	10	US-09-333-966-6
12	1484	82.3	281	9	US-09-756-854-3
13	1484	82.3	281	9	US-10-041-574-3
14	997	55.3	237	9	US-09-925-299-960
15	997	55.3	237	10	US-09-925-299-960
16	942	52.2	167	9	US-10-112-793-22
17	893	49.5	157	10	US-09-949-713-15
18	856	47.5	327	10	US-09-802-669-66
19	811.5	45.0	144	10	US-09-949-713-21

20	811.5	45.0	159	10	US-09-949-713-23	Sequence 23, Appl
21	811.5	45.0	376	10	US-09-949-713-22	Sequence 22, Appl
22	757	42.0	128	10	US-09-949-713-9	Sequence 9, Appl
23	757	42.0	143	10	US-09-949-713-10	Sequence 10, Appl
24	757	42.0	360	10	US-09-949-713-11	Sequence 11, Appl
25	712	39.5	119	9	US-10-112-793-15	Sequence 15, Appl
26	712	39.5	119	10	US-09-800-909-5	Sequence 5, Appl
27	712	39.5	119	10	US-09-884-987-3	Sequence 3, Appl
28	712	39.5	119	10	US-09-800-908-14	Sequence 14, Appl
29	579.5	32.1	204	10	US-09-948-018-18	Sequence 18, Appl
30	393	21.8	77	9	US-10-112-793-24	Sequence 24, Appl
31	386	21.4	77	9	US-09-992-964-17	Sequence 17, Appl
32	386	21.4	77	10	US-09-887-879-17	Sequence 17, Appl
33	352	19.5	68	9	US-09-756-854-22	Sequence 22, Appl
34	352	19.5	68	9	US-10-041-574-22	Sequence 22, Appl
35	328	18.2	63	12	US-10-035-408-1	Sequence 1, Appl
36	206	11.4	283	10	US-09-924-231-2	Sequence 2, Appl
37	206	11.4	283	10	US-09-934-289A-13	Sequence 13, Appl
38	206	11.4	283	10	US-09-935-727-31	Sequence 31, Appl
39	206	11.4	283	12	US-10-020-787-2	Sequence 2, Appl
40	206	11.4	283	12	US-10-066-209-2	Sequence 2, Appl
41	206	11.4	833	9	US-10-226-296-5	Sequence 5, Appl
42	206	11.4	833	9	US-10-226-318-5	Sequence 5, Appl
43	205.5	11.4	350	9	US-10-076-754-6	Sequence 6, Appl
44	205.5	11.4	350	9	US-10-076-773-6	Sequence 6, Appl
45	205.5	11.4	350	12	US-10-067-615-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-826-212-7
; Sequence 7, Application US/09826212
; Patent No. US20010021516A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; APPLICANT: NI, Jian
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280006
; CURRENT APPLICATION NUMBER: US/09/826.212
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-212-7

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Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT	120
Db	61	KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT	120
Qy	121	RTQNTKRCCKPNFCNSTVCEHCDPCTKCEHGIKECTLTNTCKCKEGSRNLGWLCLL	180
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Qy	181	LLPIPLIWWKKEVQKTCRKHKENQGSHPINLPETVAINLSDVDLSKYITTIAGVM	240
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Db 241 TLSQVGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHWLHGKKEAYDTLIKDLKK 300
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Db 301 ANLCTLAETIQTILKDTSDSENSNFRNEIQSLV 335

RESULT 2
US-09-802-669-2
; Sequence 2, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-669-2

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Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-949-713-20
; Sequence 20, Application US/09949713
; Patent No. US20020044944A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. US20020044944A1
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
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; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-713-20

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QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEGRSRLGWLCLL 180
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Db 181 LLPIPLIVWVKRVEQVTKCRKRKENGSGHESPTLPETVAIINLSVDVLSKYITTIAGVM 240

QY 241 TLSQVGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHWLHGKKEAYDTLIKDLKK 300
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RESULT 4
US-09-874-138-4
; Sequence 4, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Relner L.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/874,138
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Homo sapiens
US-09-874-138-4

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
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RESULT 5

US-09-884-987-2
Sequence 2, Application US/09884987
Patent No. US20020102653A1
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu et al
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REFERENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-884-987-2

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
DB 61 KCPGGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
DB 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
QY 181 LLPIPLVWVKRKEVQTKRKHKEGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
DB 181 LLPIPLVWVKRKEVQTKRKHKEGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300

QY 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335

RESULT 6

US-09-935-727-9
Sequence 9, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-727-9

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
DB 61 KCPGGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
DB 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
QY 181 LLPIPLVWVKRKEVQTKRKHKEGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
DB 181 LLPIPLVWVKRKEVQTKRKHKEGSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335

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Db 301 ANLCTLAETIILKDTSDSENSFRNEIQSLV 335
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RESULT 7
US-10-005-842-4
; Sequence 4, Application US/10005842
; Patent No. US20020098550A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Gentz, Reiner
; Yu, Guo-Liang
; Su, Jeffrey
; Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/005,842
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,583
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/040,846
; FILING DATE: 17-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF366
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3013098504
; TELEFAX: 3013098439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-005-842-4
Query Match 100.0%; Score 1804; DB 12; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTETQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGSRNLGWLCLL 180
QY 181 LLPIPLIIVVAKKEVQKTRKHKRKNOGSHESPTLPETVAINLSVDLSKIYITTIAGVM 240
Db 181 LLPIPLIIVVAKKEVQKTRKHKRKNOGSHESPTLPETVAINLSVDLSKIYITTIAGVM 240

QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKOLLRNWHLHGKKEAYDTLIKDLKK 300
|||||
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKOLLRNWHLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIILKDTSDSENSFRNEIQSLV 335
|||||
Db 301 ANLCTLAETIILKDTSDSENSFRNEIQSLV 335
|||||
RESULT 8
US-10-226-296-3
; Sequence 3, Application US/10226296
; Publication No. US20030036168A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Rosen, Craig A.
; Pan, James G. L.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; Receptor 4), Member of the TNF-Receptor
; Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/226,296
; FILING DATE: 23-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.13000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-226-296-3
Query Match 100.0%; Score 1804; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 2.3e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTETQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTVTETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
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QY 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKKEGSRNGLWJCLL 180
DB 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKKEGSRNGLWJCLL 180
QY 181 LLPIPLIWWKRKEVQKTCRKHKRKNQGSHPNTPETVAINLSDVLSKYIITTIAGVM 240
DB 181 LLPIPLIWWKRKEVQKTCRKHKRKNQGSHPNTPETVAINLSDVLSKYIITTIAGVM 240
QY 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQJLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQJLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIQTIIKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAEKIQTIIKDTSDSENSNFRNEIQSLV 335

RESULT 9

US-10-226-318-3
; Sequence 3, Application US/10226318
; Publication No. US20030073187A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
; Receptor 4), Member of the TNF-Receptor
; Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/226,318
; FILING DATE: 23-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-226-318-3

Query Match 100.0%; Score 1804; DB 9; Length 669;

Best Local Similarity 100.0%; Pred. No. 2.3e-130;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLGLRKTVTTVETONLEGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLGLRKTVTTVETONLEGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLCDGEGHGLEVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLCDGEGHGLEVEINCT 120
QY 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKKEGSRNGLWJCLL 180
DB 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTCKKEGSRNGLWJCLL 180
QY 181 LLPIPLIWWKRKEVQKTCRKHKRKNQGSHPNTPETVAINLSDVLSKYIITTIAGVM 240
DB 181 LLPIPLIWWKRKEVQKTCRKHKRKNQGSHPNTPETVAINLSDVLSKYIITTIAGVM 240
QY 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQJLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQJLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIQTIIKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAEKIQTIIKDTSDSENSNFRNEIQSLV 335

RESULT 10

US-09-314-889-6
; Sequence 6, Application US/09314889
; Publication No. US20030077694A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P. L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/815,469
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-314-889-6

Query Match
Best Local Similarity 99.3%; Score 1792; DB 9; Length 335;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVETQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLNGLWLCIL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLNGLWLCIL 180
QY 181 LLPIPLIVWVKKEVOKTCRKHKENQGSHPSTLNPTVAINLSDVDLSKYITTIAGVM 240
DB 181 LLPIPLIVWVKKEVOKTCRKHKENQGSHPSTLNPTVAINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETIQTILKDTSDSENSNFRNEIQSLV 335

RESULT 11
US-09-333-966-6
Sequence 6, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20020009773A1 Relevant
TOPOLOGY: No. US20020009773A1 Relevant
MOLECULE TYPE: protein
US-09-333-966-6

Query Match
Best Local Similarity 99.3%; Score 1792; DB 10; Length 335;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVETQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLNGLWLCIL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLNGLWLCIL 180
QY 181 LLPIPLIVWVKKEVOKTCRKHKENQGSHPSTLNPTVAINLSDVDLSKYITTIAGVM 240
DB 181 LLPIPLIVWVKKEVOKTCRKHKENQGSHPSTLNPTVAINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETIQTILKDTSDSENSNFRNEIQSLV 335

RESULT 12
US-09-756-854-3
Sequence 3, Application US/09756854
Patent No. US2002016484A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <Unknown>

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, PRIOR APPLICATION NUMBER: 09/124,270
, PRIOR FILING DATE: 1999-03-12
, NUMBER OF SEQ ID NOS: 1556
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 960
, LENGTH: 237
, TYPE: PRT
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: SITE
, LOCATION: (68)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
, NAME/KEY: SITE
, LOCATION: (166)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
, NAME/KEY: SITE
, LOCATION: (177)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
, NAME/KEY: SITE
, LOCATION: (187)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
, NAME/KEY: SITE
, LOCATION: (223)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
, US-09-925,299-960

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Query Match 55.3%; Score 997; DB 9; Length 237;
Best Local Similarity 96.8%; Pred. No. 4.7e-69;
Matches 179; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
|||||
DB 53 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 112
|||||

QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLXVEINCT 120
|||||

DB 113 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLXVEINCT 172
|||||

QY 121 RTQNTKCRCKPFFCNSTVCEHCDPCTKCEHGIIECTILTSNTKCKEGRSRLGLWLL 180
|||||

DB 173 RTQNTKCRCKPFFCNSTVCEHCDPCTKCEHGIIECTILTSNTKCKEGRSRLGLWLL 232
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QY 181 LLPIP 185
|||||

DB 233 LLPIP 237
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Search completed: May 9, 2003, 17:09:07
Job time : 20.6994 secs

RESULT 15
US-09-925-299-960
; Sequence 960, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05983
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 960
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (68)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (166)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (177)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (223)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-960

Query Match 55.3%; Score 997; DB 10; Length 237;
Best Local Similarity 96.8%; Pred. No. 4.7e-69;
Matches 179; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
|||||

DB 53 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 112
|||||

QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLXVEINCT 120
|||||

DB 113 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLXVEINCT 172
|||||

QY 121 RTQNTKCRCKPFFCNSTVCEHCDPCTKCEHGIIECTILTSNTKCKEGRSRLGLWLL 180
|||||

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:02:31 ; Search time 28.8444 seconds
(without alignments)
1116.509 Million cell updates/sec

Title: US-09-446-634A-22
Perfect score: 1804
Sequence: 1 MGIWTLPLVLTSSVARLSS.....KDITSDSENSFRNEIQSLV 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1804	100.0	335	2	A40036	apoptosis-mediating
2	1667.5	92.4	314	2	I37383	FAS soluble protei
3	856	47.5	327	2	A46484	apoptosis-mediati
4	827.5	45.9	324	2	JC2395	Fas antigen precu
5	621.5	34.5	149	2	S58662	Fas-Delta-(4,7) pr
6	342.5	19.0	103	2	I37384	FAS soluble protei
7	185.5	10.3	435	2	I54182	tumor necrosis fac
8	182	10.1	416	1	JN0006	nerve growth facto
9	177	9.8	455	1	GQHUT1	tumor necrosis fac
10	173.5	9.6	305	2	A46476	B cell-associated
11	164.5	9.1	250	1	A49053	CD27 antigen precu
12	161.5	9.0	277	2	A60771	B-cell activation
13	161	8.9	461	2	JC4302	tumor necrosis fac
14	159.5	8.8	260	1	A46517	CD27 antigen precu
15	159	8.8	427	1	GQHUN	nerve growth facto
16	156	8.6	425	1	A26431	nerve growth facto
17	146	8.1	454	1	GQMST1	tumor necrosis fac
18	144	8.0	272	2	I48700	gene ox40 protein
19	141.5	7.8	271	2	S12783	ox40 antigen precu
20	141.5	7.8	461	1	A35356	tumor necrosis fac
21	141	7.8	349	2	D72175	G2R protein - vari
22	139	7.7	348	2	T28623	hypothetical prote
23	139	7.7	349	2	T28658	gene CAR protein -
24	136.5	7.6	383	2	S53716	delta-like homeoti
25	131.5	7.3	385	2	A54785	preadipocyte facto
26	131.5	7.3	2180	2	T29764	hypothetical prote
27	130.5	7.2	677	2	C42125	trophozoite cystei
28	129.5	7.2	326	1	GQVZML	T2 protein - myxom
29	129.5	7.2	385	2	S53718	homeotic protein d

30	128	7.1	728	2	I50719	C-Delta-1 - chicke
31	125.5	7.0	574	2	B88465	protein B0244.8 [i
32	125	6.9	1014	2	T30545	major surface glyco
33	124.5	6.9	325	2	B43692	T2 protein - rabbi
34	122.5	6.8	461	1	GQRTT1	tumor necrosis fac
35	121.5	6.7	474	2	B38634	tumor necrosis fac
36	121.5	6.7	1766	2	A42125	trophozoite cystei
37	120.5	6.7	277	2	I37552	OX40 homolog - hum
38	120.5	6.7	459	2	I48854	gene murine tumour
39	119.5	6.6	1274	2	T42017	cytochrome rich prot
40	119	6.6	577	2	A60501	thrombomodulin pre
41	118.5	6.6	1786	1	MMHUB1	laminin beta-1 cha
42	117.5	6.5	1111	2	T26972	hypothetical prote
43	115.5	6.4	1372	2	T25933	hypothetical prote
44	115	6.4	1104	2	I38869	transcription fact
45	114.5	6.3	1816	1	S68960	laminin alpha-4 ch

ALIGNMENTS

RESULT 1

A40036
apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1
C:Species: Homo sapiens (man)
C>Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C:Accession: A40036; S24543; A38142
R:Itch, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; H
Cell 66, 233-243, 1991
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can
A:Reference number: A40036; MUID:91309137; PMID:1713127
A:Accession: A40036
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <ITD>
A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
R:Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A:Reference number: S24543
A:Accession: S24543
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <KRA>
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Mair, G.; Klas, C.; Li-Weber, M.;
J. Biol. Chem. 267, 10709-10715, 1992
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a mem
A:Reference number: A38142; MUID:92268122; PMID:1375228
A:Accession: A38142
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-134, 'Q', 136-335 <OE>
A:Experimental source: SKW6.4 cells
A>Note: sequence extracted from NCBI backbone (NCBIP:103810)
A>Note: in NCBI backbone the source is designated as mouse
C:Genetics:
A:Gene: GDB:APF1
A:Cross-references: GDB:132671; OMIM:134637
A:Map position: 10q24.1-10q24.1
C:Superfamily: NGF receptor repeat homology
C:Keywords: apoptosis; surface antigen; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:85-128/Domain: NGF receptor repeat homology <NG4>
F:174-190/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 1804; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 5e-118;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSSVARLSSVNAQVTDINSKGLRKTVTVTQNLGLHHDQFCH 60
DB 1 MGIWTLPLVLTSSVARLSSVNAQVTDINSKGLRKTVTVTQNLGLHHDQFCH 60

DB I MLGIWTLPLVLT\$VARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLGLHHDGQFCH 60

Query Match 9.8%; Score 177; DB 1; Length 455;
Best Local Similarity 21.7%; Pred. NO. 5.8e-05;
Matches 97; Conservative 37; Mismatches 153; Indels 150; Gaps 18;

```

Db 10 LLPLVLELLVGYPSGVLGPHLGDGR--EKRDSCVPOGKYIHQN-----NSICT 60
QY 62 PCPPGPKARDCTVNGDEPCVPCQSGKEYTDKAHF-----SKKRR----- 103
Db 61 KCHKYIYLYNDCPGQODTDCRECSGSPFASENHLRHCLSCSKCKEMQVEISSCTVD 120
QY 104 -----CRLCDDEGHGLVEINCTRTQNTKCRKXPNFCNFT 138
Db 121 RDTVCGRKNQYRHYWSENLFQFCNGSLCLNG---FVHLSCQEKQNTVCTCHAGFRLRN 177
QY 139 VCEHCDPCTKCEHGIKECT-----LTSNTCKKEGSRNL-----GWLCLL-LLPIPL 186
Db 178 ECVSCSNCKKS-----LECTKLCLPQIENVKGTEDSGTTLVPLVTFGGLCLLSLLFLG 232
QY 187 IV----WVKRKEVQKTCRKHRKENOGSHESPTLNP-----ETVAINLSDVDLS 230
Db 233 MYRYQRW-KSKLISYVCGKSTPEKEGELEGTTKPLAPNPSPTPGFTPLGFSVPSS 291
QY 231 KY-----ITTIAG----- 238
Db 292 TFTSSSTYTPGDCPNFAAPRREVAPPYQAGDPIALATALASDPTPNPLQKWECSAHPQSL 351
QY 239 ----VMTLSQV-----KGFVRKNGVNEAKIDIKNDNVQDTAEQKVOLLRNHQHL 285
Db 352 DTDDPATLYXAVENVPLRWKEFVRGLGSDHEIDRLLEQLONGRLCREAOYSMLATWRRRT 411
QY 286 GKKEA-YDTLILKIDKLKKNLCTLAEKIQ 311
Db 412 PREANTLELLGRVLRDMDLLGCLIEDIE 438

RESULT 10
A6476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A64676; A46515
J. Immunol. 148, 620-626, 1992
R:Torres, R.M.; Clark, E.A.
A:Title: Differential increase of an alternatively polyadenylated mRNA spe
A:Reference number: A64676; MUID:92105763; PMID:1370315
A:Accession: A6476
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:g1553058
A>Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A>Note: this translation is not annotated in GenBank entry MUSCD40A, relea
J. Grimaldi, J.C.; Torres, R.; Kosak, C.A.; Chang, R.; Clark, E.A.; Howard,
R. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene
A:Reference number: A46515; MUID:93094586; PMID:12811194
A:Accession: A46515
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287,'LV' <GR>
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059
A:Experimental source: BALB/c, liver
A>Note: sequence extracted from NCBI backbone (NCBIP:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

```

Query Match	9.6%	Score 173.5;	DB 2;	Length 305;
Best Local Similarity	33.1%;	Pred. No. 6.8e-05;		
Matches 44:	Conservative	19;	Mismatches 61;	Indels 9;
				Gaps 5;

Qy 35 LELRKTVTTVETQNLEGLHHGQFCHKKPPGERKARDCTVNGDEPDVCVPQCQEKEYTDK 94
:
db 18 VHLGOCVTCSDKOYL-----HDGCCDL-COPGSRUTSHCTAL-EKTOCHPCDSG-EFSAQ 70
:

```

C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          9.0%; Score 161.5; DB 2; Length 277;
Best Local Similarity 26.3%; Pred. No. 0.00042;
Matches 66; Conservative 31; Mismatches 89; Indels 65; Gaps 14;

QY  59  CHKPCPPGKARKDVTNGDEPCVPCQSGKEYTKAHFSSKRCRCDCDEGHGLEVIN 118
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   37  CCSLQPGQQLVSDCT-ETETECPCGE-SFLDTWNRETHCHQHKYCDPNLGRVQOK  94
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  119  CTRTQNTKCRKNFFCNSTVCEHCDPCKCEHGI-IKE-CTLTNTKCK--EEGRSNL 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   95  GTSETDITCTCEGWHCSTSEACSVLHSCSPGFGVKQIATGVSDTICEPCPVGFSSNV 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  175  G-----W-----LC-----LLLLPI-----PLIVVVK 191
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   155  SSAFEKCHPWTSCTKDLVVOAGTNKTDVCGPDRLRALVPIPIFGILFAILLVLF 214
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  192  RKEVQKTRKRRKNGSHESPTLNPTVAIINLSDVLSKYIT-----TIAGVMTLSQV 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   215  IKVKV-----KPTNKAPH--PKQEPQ--EINFPD-DLPGSNTPAAVQETHLGCQPVQ 264
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  246  KGFVRKNGVNE 256
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   265  DGRSRLSVOE 275
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 13
JC4302

tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor
A:Reference number: JC4302; MUID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: GB:U19994; NID:gl141752; PIDN:AAC48499.1; PID:gl141753
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-20/domain: signal sequence #status predicted <SIG>
F:30-461/product: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-194/domain: extracellular cysteine rich #status predicted <EXP>
F:44-82/domain: NGF receptor repeat homology <NG1>
F:84-126/domain: NGF receptor repeat homology <NGF>
F:211-231/domain: transmembrane #status predicted <TMW>
F:361-447/domain: signal transduction #status predicted <SIT>
F:54.145/151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.9%; Score 161; DB 2; Length 461;
Best Local Similarity 18.6%; Pred. No. 0.00076;
Matches 86; Conservative 45; Mismatches 147; Indels 184; Gaps 15;

[illegible]

RESULT 14
A46517
CD27 antigen precursor - human
N:Alternate names: CD27L receptor; T cell activation antigen CD27
C:Species: Homo sapiens (man)
C:Date: 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
C:Accession: A46517; A46454
R:Loenen, W.A.; Gravesstein, L.A.; Beumer, S.; Melief, C.J.; Hagemeijer, A.; Borst, J.
J. Immunol. 149, 3937-3943, 1992
A:Title: Genomic organization and chromosomal localization of the human CD27 gene.
A:Reference number: A46517; MUID:93094588; PMID:1334106
A:Accession: A46517
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-260 <LOE>
A:Note: sequence extracted from NCBI backbone (NCBIP:120386)
A:Note: authors propose an alternative repeat pattern
R:Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.
J. Immunol. 147, 3165-3169, 1991
A:Title: The T cell activation antigen CD27 is a member of the nerve growth factor/tumor
A:Reference number: A46454; MUID:92013149; PMID:1655907
A:Accession: A46454
A:Molecule type: mRNA
A:Residues: 1-58, 'A', 60-260 <CAM>
A:Cross-references: GB:M63928; NID:gl80084; PIDN:AAA58411.1; PID:gl80085
A:Note: sequence extracted from NCBI backbone (NCBIN:60285, NCBIP:60289)
C:Comment: A soluble CD27 found in serum and urine is formed by proteolysis.

[illegible]

RESULT 15

GOHUN

nerve growth factor receptor precursor, low affinity [validated] - human

N;Alternate names: NGF receptor

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1988 #sequence-revision 31-Mar-1988 #text_change 08-Dec-2000

C;Accession: A5218; A60204; S21689; I57638

R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E. E. Cell 47, 545-554, 1986

A;Title: Expression and structure of the human NGF receptor.

A;Reference number: A25218; MUID:87051725; PMID:3022937

A;Accession: A25218

A;Molecule type: mRNA

A;Residues: 1-427 <JOH>

A;Cross-references: GB:M14764; NID:gl89204; PIDN:AAE59544.1; PID:gl89205

R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattman, G.; Thompson, J. Neurochem. 48, 225-232, 1987

A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor.

A;Reference number: A60204; MUID:87085574; PMID:3025363

A;Accession: A60204

A;Molecule type: protein

A;Residues: 29-31,'N',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>

A;Experimental source: melanoma cell line A875

A;Note: This sequence has been corrected by a note added in proof to follow Arch. Biochem. Biophys. 294, 244-252, 1992

R;Vissavajhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.

A;Title: Structural domains of the extracellular domain of human nerve growth factor.

A;Reference number: S21689; MUID:92198017; PMID:1372492

A;Accession: S21689

A;Status: preliminary

A;Molecule type: Protein

R;Sehgal, A.; Patil, N.; Chao, M. Mol. Cell. Biol. 8, 3160-3167, 1988

A;Title: A constitutive promoter directs expression of the nerve growth factor gene.

A;Reference number: I57638; MUID:89096903; PMID:2850481

A;Accession: I57638

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-22 <RSS>

A;Cross-references: GB:M21621; NID:gl89206; PIDN:AAA36363.1; PID:gl89207

C;Comment: This receptor is found on sensory and sympathetic neurons, on nerve growth factor receptor, glycoprotein; heterodimer; monomer; phosphoprotein

C;Comment: The cysteine-rich region of the extracellular domain may form a high-affinity receptor when I

C;Comment: This receptor undergoes both N- and O-linked glycosylation.

C;Genetics:

A;Gene: GDB:NGFR

A;Cross-references: GDB:120234; OMIM:162010

A;Map position: 17q21-17q22

C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein

F;1-28/Domain: signal sequence #status predicted <SIG>

F;29-42/Product: nerve growth factor receptor #status experimental <MAT>

F;29-250/Domain: extracellular #status predicted <EXT>

F;32-65/Domain: NGF receptor repeat homology <NGI>

F;67-108/Domain: NGF receptor repeat homology <NGD>

Search completed: May 9, 2003, 17:07:52
Job time : 31.8444 secs

GenCore version 5.1.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:58:17 ; Search time 15.6873 Seconds
(without alignments)
885.720 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804

Sequence: 1 MGIWTLPLVLTSVARLSS.....KDTSDSENSFNERIQSLV 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	335	1 TNR6_HUMAN	P25445 homo sapien
2	1029.5	57.1	332	1 TNR6_PIG	O77736 sus scrofa
3	951	52.7	323	1 TNR6_BOVIN	P51867 bos taurus
4	856	47.5	327	1 TNR6_MOUSE	P25446 bos taurus
5	827.5	45.9	324	1 TNR6_RAT	O63199 rattus norv
6	211.5	11.7	381	1 T10B_MOUSE	O9qzm4 mus musculus
7	206	11.4	283	1 TR14_HUMAN	Q92956 homo sapien
8	199.5	11.1	417	1 TR12_HUMAN	Q93038 h tumor nec
9	197.5	10.9	468	1 T10A_HUMAN	O00220 homo sapien
10	197	10.9	440	1 T10B_HUMAN	O14763 homo sapien
11	189.5	10.5	176	1 TR23_MOUSE	O9er63 mus musculus
12	186	10.3	401	1 T11B_RAT	O08727 rattus norv
13	185.5	10.3	435	1 TNR3_HUMAN	P36941 homo sapien
14	183	10.1	401	1 T11B_HUMAN	O00300 homo sapien
15	182	10.1	401	1 T11B_MOUSE	O08712 mus musculus
16	182	10.1	416	1 TR16_CHICK	P18519 gallus gall
17	180	10.0	180	1 TR22_MOUSE	O9er62 mus musculus
18	177	9.8	455	1 TR1A_HUMAN	P19438 homo sapien
19	173.5	9.6	289	1 TNR5_MOUSE	P27512 mus musculus
20	169	9.4	386	1 T10D_HUMAN	Q9ubn6 homo sapien
21	164.5	9.1	250	1 TNR7_MOUSE	P41272 mus musculus
22	163.5	9.1	259	1 T10C_HUMAN	O14798 h tumor nec
23	161.5	9.0	277	1 TNR5_HUMAN	P25942 homo sapien
24	161	8.9	461	1 TR1A_PIG	P50555 sus scrofa
25	159.5	8.8	260	1 TNR7_HUMAN	P26842 homo sapien
26	159	8.8	427	1 TR16_HUMAN	P08138 homo sapien
27	156	8.6	425	1 TR16_RAT	P07174 rattus norv
28	153	8.5	349	1 CRMB_CAMPS	O8uya7 camelpox vi
29	151	8.4	417	1 TR16_MOUSE	O9z0w1 mus musculus
30	148.5	8.2	351	1 CRMB_COWPX	O73559 cowpox viru
31	147	8.1	415	1 TNR3_MOUSE	P50284 mus musculus
32	147	8.1	471	1 TR1A_BOVIN	O19131 bos taurus
33	146	8.1	454	1 TR1A_MOUSE	P25118 mus musculus

34	145	8.0	300	1 TR6B_HUMAN	O95407 homo sapien
35	144	8.0	272	1 TNR4_MOUSE	P47741 mus musculus
36	141.5	7.8	271	1 TNR4_RAT	P15725 rattus norv
37	141.5	7.8	461	1 TR1B_HUMAN	P20333 homo sapien
38	139	7.7	349	1 CRMB_VARV	P34015 variola vir
39	137.5	7.6	269	1 TNR5_BOVIN	Q28203 bos taurus
40	136.5	7.6	383	1 DLK_HUMAN	P80370 homo sapien
41	135	7.5	616	1 TR11_HUMAN	Q9y6q6 homo sapien
42	134.5	7.5	625	1 TR11_MOUSE	O35305 mus musculus
43	129.5	7.2	326	1 VT2_MXVVL	P29825 myxoma viru
44	129.5	7.2	385	1 DLK_MOUSE	Q99163 mus musculus
45	124.5	6.9	325	1 VT2_SFVKA	P25943 Shope fibro

ALIGNMENTS

RESULT 1
TNR6_HUMAN
ID TNR6_HUMAN STANDARD; PRT; 335 AA.
AC P25445; Q14293; Q14294; Q14295; Q14292; Q16652;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
DE (CD95).
GN TNFRSF6 OR A2T1 OR FAS OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91309137; PubMed=1713127;
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I., Sameshima M., Hase A., Seto Y., Nagata S.;
RA "The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis.";
RT Cell 66:233-243(1991).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX MEDLINE=92263122; PubMed=1375228;
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C., Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H., Krammer P.H.;
RA "Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen.";
RT J. Biol. Chem. 267:10709-10715(1992).
RL [3]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.
RX MEDLINE=95181785; PubMed=753181;
RA Cascino I., Fucci G., Papoff G., Ruberti G.;
RA "Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing.";
RT J. Immunol. 154:2706-2713(1995).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM 5).
RX TISSUP-Peripheral blood lymphocytes;
RA Schaezlein C.E., Poehlmann R., Philippssen P., Eibel H.;
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
RX MEDLINE=96238926; PubMed=8648105;
RA Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;
RA "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants prevents cell death in vitro.";
RT J. Immunol. 156:4622-4630(1996).
RN [6]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE-Urinary bladder;


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Query Match 100.0%; Score 1804; DB 1; Length 335;
Best Local Similarity 100.0%; Pred No. 3.9e-128;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTQNLGLHHGQFCH 60
DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTQNLGLHHGQFCH 60

QY 61 KPCPPGERKADCTVNGDEPCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 120
DB 61 KPCPPGERKADCTVNGDEPCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 120

QY 121 RTQNTKCRCKPNFCHTSCHECHDPCCTKCEHGIIEKCTLSNTKCKEGRSRLGLWCLL 180
DB 121 RTQNTKCRCKPNFCHTSCHECHDPCCTKCEHGIIEKCTLSNTKCKEGRSRLGLWCLL 180

QY 181 LLPIPLIIVWKRKEVQKTCRRKRKENGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240
DB 181 LLPIPLIIVWKRKEVQKTCRRKRKENGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240

QY 241 TISOVKGFVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNWHQHLHGKKEAYDTLIKDLKK 300
DB 241 TISOVKGFVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNWHQHLHGKKEAYDTLIKDLKK 300

QY 301 ANLCTLAETIILKIDTSDSENSFRNEIQSLV 335
DB 301 ANLCTLAETIILKIDTSDSENSFRNEIQSLV 335

RESULT 2
TNR6_PIG STANDARD; PRT; 332 AA.
ID TNR6_PIG STANDARD; PRT; 332 AA.
AC 077736; 1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNR6SF6 OR APT1 OR FAS.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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DR EMBL; AJ001202; CAA04596.1; -.
DR HSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS00050; TNFR_NGFR_3; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 332
FT DOMAIN 17 175
FT TRANSMEM 176 192
FT DOMAIN 193 332
FT REPEAT 45 81
FT REPEAT 82 125
FT REPEAT 126 164
FT DOMAIN 227 311
FT DISULFID 46 57
FT DISULFID 58 71
FT DISULFID 61 80
FT DISULFID 83 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 141
FT DISULFID 144 155
FT DISULFID 147 163
FT CARBOHYD 38 38
FT CARBOHYD 116 116
FT SEQUENCE 332 AA; 37592 MW; 588B03682756BFIB CRC64;
Query Match 57.1%; Score 1029.5; DB 1; Length 332;
Best Local Similarity 59.1%; Pred. No. 3.8e-70;
Matches 201; Conservative 50; Mismatches 74; Indels 15; Gaps 7;
QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTQNLGLHHGQFCH 60
DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTQNLGLHHGQFCH 60
QY 61 KPCPPGERKADCTVNGDEPCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 120
DB 61 KPCPPGERKADCTVNGDEPCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 120
QY 59 QPCPPGERKADCTVNGDEPCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 118
DB 59 QPCPPGERKADCTVNGDEPCVPCQEGKEYTDKAHSSKRCRRCLDEGHGVEINCT 118
QY 121 RTQNTKCRCKPNFCHTSCHECHDPCCTKCEHGIIEKCTLSNTKCKEGRSRLGLWCLL 176
DB 121 RTQNTKCRCKPNFCHTSCHECHDPCCTKCEHGIIEKCTLSNTKCKEGRSRLGLWCLL 176
QY 177 L--CLLLPIPLIIVWKRKEVQKTCRRKRKENGSHESPTLPETVAINLSDVDLSKYIT 234
DB 177 L--CLLLPIPLIIVWKRKEVQKTCRRKRKENGSHESPTLPETVAINLSDVDLSKYIT 234
QY 179 L--CLLLPIPLIIVWKRKEVQKTCRRKRKENGSHESPTLPETVAINLSDVDLSKYIT 231
DB 179 L--CLLLPIPLIIVWKRKEVQKTCRRKRKENGSHESPTLPETVAINLSDVDLSKYIT 231
QY 235 TIAGVMTLSQVKGKGFVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNWHQHLHGKKEAYDTL 294
DB 235 TIAGVMTLSQVKGKGFVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNWHQHLHGKKEAYDTL 294
QY 232 RIAGQNKITEVQKGFVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNWHQHLHGKKEAYDTL 291
DB 232 RIAGQNKITEVQKGFVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNWHQHLHGKKEAYDTL 291
QY 295 IKDLKKNALCTLAETIILKIDTSDSENSFRNEIQSL 334
DB 295 IKDLKKNALCTLAETIILKIDTSDSENSFRNEIQSL 334
QY 292 IQGLRKAALADKINDIVQKDVTSQENANSQENESL 331
DB 292 IQGLRKAALADKINDIVQKDVTSQENANSQENESL 331
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RESULT 3
TNR6_BOVIN STANDARD; PRT; 323 AA.
ID TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE
```

DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226401; PubMed=8634151;
RA Yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234(1996).
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
CC DR EMBL; U34794; AAC48546.1; --
CC DR HSPSP; P25445; IDDF.
CC DR InterPro; IPR000488; Death.
CC DR InterPro; IPR001369; TNFR_C6.
CC DR Pfam; PF00020; TNFR_C6; 3.
CC DR Pfam; PF00531; death; 1.
CC DR SMART; SM00005; DEATH; 1.
CC DR SMART; SM00208; TNFR; 3.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE; PS00652; TNFR_NGFR_2; 2.
CC DR PROSITE; PS50050; TNFR_NGFR_1; 1.
CC DR PROSITE; PS50017; DEATH_DOMAIN; 1.
CC KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
CC FT SIGNAL 1 16 POTENTIAL.
CC FT CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
CC FT 17 323 SUPREAFAMILY MEMBER 6.
CC FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 171 188 POTENTIAL.
CC FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
CC FT REPEAT 45 80 TNFR-CYS 1.
CC FT REPEAT 81 124 TNFR-CYS 2.
CC FT REPEAT 125 163 TNFR-CYS 3.
CC FT DOMAIN 238 306 DEATH.
CC FT DISULFID 45 56 BY SIMILARITY.
CC FT DISULFID 57 70 BY SIMILARITY.
CC FT DISULFID 60 79 BY SIMILARITY.
CC FT DISULFID 82 98 BY SIMILARITY.
CC FT DISULFID 101 116 BY SIMILARITY.
CC FT DISULFID 104 124 BY SIMILARITY.
CC FT DISULFID 126 140 BY SIMILARITY.
CC FT DISULFID 143 154 BY SIMILARITY.
CC FT DISULFID 146 162 BY SIMILARITY.
CC FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 115 115 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;

Query Match 52.7%; Score 951; DB 1; Length 323;
Best Local Similarity 56.8%; Pred No. 2.8e-64;
Matches 191; Conservative 47; Mismatches 84; Indels 14; Gaps 6;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLKELRTVTVTQNLGLHHDGQFCH 60
Db 1 MSGIWWHLISLIPISVSGPLSKGENAHMAGINSEGLKLN---ITEANSQCEGLYREHFQCC 57
QY 61 KPCPGPKRKARDCTVNGDEPCVQCEQGEKYTDKAHFSKRCRCRLCDHGHEVEINCT 120
Db 58 QPCPGPKRNGDKRGGDTPECVLCSENGEYTDKSHHSDKRCISCDDEHGLEVEQNC 117
QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIIEKCTILTSNTKCKEGRSRLGW-LCL 179
Db 118 RTRNTKCRCKSNFFCNSSPCEHCNCTTCEHGIIEKCTPTNTKCKGSRSHANSWALLI 177
QY 180 LLIPPLIPLVWKRKEVQYCKRKHENOGSHESPLNPETVAINLSDVLSKYITTIAGV 239
Db 178 LLIPPLIPLVLIY---KVKRS-REKKNKDYCN-SASNDDEGRQLNLTVDLGRYIPSAEQ 231
QY 240 MTLQVQKGFVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHOLGHGKEAYDTLIKDK 299
Db 232 MRITVEKFEVRKNGMEAEKIDIDHDNVHETAEQVQLLRNWHYSHGKKNAYCTLTSLP 291
QY 300 KANLCTLAETQTLIKDITSDSENSFNRIQSLV 335
Db 292 KA----LAETICDIVMKDITNERENANIQENENLV 323

RESULT 4
ID TNFR6_MOUSE STANDARD; PRT; 327 AA.
AC P25446; Q9DCQ1;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92148151; PubMed=1371136;
RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.;
RA Copeland N.G., Jenkins N.A., Nagata S.;
RT "The cDNA structure, expression, and chromosomal assignment of the
RT mouse Fas antigen.";
RL J. Immunol. 148:1274-1279(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Koczan D., Ibrahim S.M., Thiesen H.J.;
RT "Role of a mutant fas receptor in a transgenic mouse.";
RN Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."; [4]
RL Nature 409:685-690(2001).
RN
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE-93189576; PubMed-7680478;
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT "Aberrant transcription caused by the insertion of an early
RT transposable element in an intron of the Fas antigen gene of lpr
RT mice."; [5]
RN Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RP VARIANT LPR
RX MEDLINE-92195401; PubMed-1372394;
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Nagata S.;
RT "Lymphoproliferation disorder in mice explained by defects in Fas
RT antigen that mediates apoptosis."; [5]
RL Nature 356:314-317(1992).
RN
RP
RX
CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (by similarity).
CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC LIVER, LUNG, HEART, AND ADULT OVARY.
CC
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC
CC -1- DISEASE: DEFECTS IN TNFSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC PRODUCTION.
CC
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC -----
CC EMBL; M83649; AAA37593.1; -;
CC EMBL; AK002590; BAB22211.1; -;
CC EMBL; AJ295702; CAC00638.1; -;
CC EMBL; AJ295703; CAC00638.1; JOINED.
CC EMBL; AJ295704; CAC00638.1; JOINED.
CC EMBL; S56490; AAB25700.1; -;
CC EMBL; S56485; AAB25700.1; JOINED.
CC EMBL; S56486; AAB25700.1; JOINED.
CC EMBL; S56487; AAB25700.1; JOINED.
CC EMBL; S56488; AAB25700.1; JOINED.
CC EMBL; S56489; AAB25700.1; JOINED.
CC EMBL; S56490; AAB25700.1; JOINED.
CC EMBL; S56491; AAB25700.1; JOINED.
CC EMBL; S56492; AAB25700.1; JOINED.
CC EMBL; S56493; AAB25700.1; JOINED.
CC EMBL; S56494; AAB25700.1; JOINED.
CC EMBL; S56495; AAB25700.1; JOINED.
CC EMBL; S56496; AAB25700.1; JOINED.
CC EMBL; S56497; AAB25700.1; JOINED.
CC EMBL; S56498; AAB25700.1; JOINED.
CC EMBL; S56499; AAB25700.1; JOINED.
CC EMBL; S56500; AAB25700.1; JOINED.
CC EMBL; S56501; AAB25700.1; JOINED.
CC EMBL; S56502; AAB25700.1; JOINED.
CC EMBL; S56503; AAB25700.1; JOINED.
CC EMBL; S56504; AAB25700.1; JOINED.
CC EMBL; S56505; AAB25700.1; JOINED.
CC EMBL; S56506; AAB25700.1; JOINED.
CC EMBL; S56507; AAB25700.1; JOINED.
CC EMBL; S56508; AAB25700.1; JOINED.
CC EMBL; S56509; AAB25700.1; JOINED.
CC EMBL; S56510; AAB25700.1; JOINED.
CC EMBL; S56511; AAB25700.1; JOINED.
CC EMBL; S56512; AAB25700.1; JOINED.
CC EMBL; S56513; AAB25700.1; JOINED.
CC EMBL; S56514; AAB25700.1; JOINED.
CC EMBL; S56515; AAB25700.1; JOINED.
CC EMBL; S56516; AAB25700.1; JOINED.
CC EMBL; S56517; AAB25700.1; JOINED.
CC EMBL; S56518; AAB25700.1; JOINED.
CC EMBL; S56519; AAB25700.1; JOINED.
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the rat liver."
RL Biochem. Biophys. Res. Commun. 198;666-674(1994).
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
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CC HSSP; P25445; 1DDF.
CC InterPro; IPR000488; Death.
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CC DISULFID 145 162 BY SIMILARITY.
CC CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 324 AA; 36835 MW; D25D583C909D9D09 CRC64;
Query Match 45.9%; Score 827.5; DB 1; Length 324;
Best Local Similarity 49.0%; Pred. No. 4.9e-55;
Matches 164; Conservative 55; Mismatches 103; Indels 13; Gaps 4;
Qy 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLERKTVTTVTQNLGLHHDGQFCH 60
Db 1 MLNIAVPLVLAG-----PELNVRMQGTDTSIFEGLELRKSVRETDNNCSGLYQVGPECC 56
Qy 61 KPCPPGERKARDVNGDEPCVQCEKGVTDKRAHSSKRCRLCDGEGHLEVNCT 120
Db 57 QPCQPGERKVKDCTTSGAPCHCTGEGEYTDKRRKSDKRCRCAFCDEGHLEVNCT 116
Qy 121 RTQNTKCRKRPNFFCNSTVCEHCDPCKCE-HGIKECTLTSTNTKCEGSRSLNGLWCL 179

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Db 117 RTQNTKCRKRENYCNASLCHYCTSCGLEDELPCTRTSNTKCKQSSNYKLW--L 174
Qy 180 LLLPIPLIYVWRKVEQKTCRKRKHNQCSHESPTLNPTVAINLSDVLSKVIITGAV 239
Db 175 LILPLGLAILEV-----FIYKRYKRQPDPSGIPSPESVPMNVSDVNLNKIYRTAEK 228
Qy 240 MTLQVKGFEVRNGVNEAKIDEIKNDVQDTAEQKVOLLRNHQLHGKKEAYDTLKLK 299
Db 229 MKICDAKFAHQHKIPESKIDIEHNSPDAAEQIKLQLQCYQSHGKTGACQALQIGUR 288
Qy 300 KANLCTLAEKIQTILKIDTSDSENSRNFEIQL 334
Db 289 KANRCIDIAETQAVYWEHENSINSRNENEGQSL 323

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RESULT 6

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T10B_MOUSE
ID T10B_MOUSE STANDARD; PRT; 381 AA.
AC Q9Q2M4; Q9JUL5; Q9JUL6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death
DE receptor 5) (MK).
GN TNFRSF10B OR DR5 OR KILLER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99310501; PubMed=10383128;
RA Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
RT "Molecular cloning and functional analysis of the mouse homologue of
RT the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand
RT (TRAIL) death receptor.";
RL Cancer Res. 59:2770-2775(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Nakamura Y., Tamari M., Watanabe O.;
RT "Mouse TRAIL receptor.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
CC adaptor molecule FADD recruits caspase-8 to the activated
CC receptor. The resulting death-inducing signaling complex (DISC)
CC performs caspase-8 proteolytic activation which initiates the
CC subsequent cascade of caspases (aspartate-specific cysteine
CC proteases) mediating apoptosis. Promotes the activation of NF-
CC kappaB.
CC -!- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
CC -!- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF176833; AAD52656.1; -
CC EMBL; AB031081; BAA96462.1; -
CC EMBL; AB031082; BAA96463.1; -
CC HSSP; O14763; 1D0G.
CC MGI; 1341090; Tnfrsf10b.

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DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR.1; FALSE_NEG.
DR PROSITE: PS00050; TNFR_NGFR.2; 2.
KW Receptor; Apoptosis; Transmembrane; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 53 381
FT FT
FT FT
FT DOMAIN 53 160
FT TRANSMEM 161 181
FT DOMAIN 182 381
FT REPEAT 26 86
FT REPEAT 87 129
FT REPEAT 130 169
FT DOMAIN 273 356
FT DISULFID 74 85
FT DISULFID 88 105
FT DISULFID 108 121
FT DISULFID 111 129
FT DISULFID 131 145
FT DISULFID 148 161
FT DISULFID 151 169
FT CONFLICT 42 42
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 180 180
FT CONFLICT 187 187
FT CONFLICT 215 215
FT CONFLICT 229 229
FT CONFLICT 306 306
SQ SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;

Query Match 11.7%; Score 211.5; DB 1; Length 381;
Best Local Similarity 24.2%; Pred. No. 7.7e-09;
Matches 72; Conservative 39; Mismatches 133; Indels 53; Gaps 10;

QY 62 PCPGERKARDCTVNGDEPCVPCQEGKEYTDKA-HFFSKRCRRCLDGEHGLEVEINCT 120
DB 73 PCLAGQVLS-----EGNCKPCREGIDYTSNHSNLDSCILCTVCKEDK--VVETRCN 122
QY 121 RTQNTKCRKPNFFCNSTVCCHDCPTCKCEHG--IIRECTLTSTNFKCEE---GSRNIG 175
DB 123 ITTWVCRKPGTFEDKDSPEICOSCNCSDGEEELTSCTPRENKCVSKTAWASWHKLG 182
QY 176 WLCLLLLP-----PLIYW-----VKR-----KEYQKTCRK 201
DB 183 LWIGLLVPVLLGALLVWKGTAMQWLLCIKRCRDPESANSVHLSLLDRQTSSTND 242
QY 202 HRKENQSHSPTLNPTVAINLSDV--DLISKYITTTAGVMTLSQVGFVRKNGVNEAKI 259
DB 243 SNHNTEPGTKTKTKLLKLLPVVNGNSADDLKAFIEYCSDIVPFDPSWNRMLRMLQGLTDNQI 302
QY 260 DEIKNDNVQDTAEQKVOLLNRNWHLGKKEAYDPLIKDLKKANLCTLAETIOTILK 316
DB 303 QMVRKATLV-TREALYQMLLKWRIQTGRSASINHLDALEAVEERDAEMEKIEDYAVK 358

RESULT 7
TR14 HUMAN STANDARD; PRT; 283 AA.
AC Q92956; Q9UM65; Q9GJ31; Q8WXRI;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor
DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
DE (TR2).
GN TNFRSF14 OR HVEM OR HVEA.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=97053782; PubMed=8898196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RL the TNF/NGF receptor family.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97306336; PubMed=9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
Porter T.G., Truneh A., Young P.R.;
RA "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RL lymphocyte activation.";
RN [3]
RP SEQUENCE FROM N.A.
RX Zhang W., Wan T., Cao X.;
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. AND VARIANTS ARG-17 AND ILE-241.
RX MEDLINE=21629477; PubMed=11756979;
RA Struyf F., Posavac C.M., Keyaerts E., Van Ranst M., Corey L.,
Spear P.G.;
RA "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT Nectin-1, and Nectin-2 in immune seronegative individuals.";
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
RX MEDLINE=21403266; PubMed=11511370;
RA Carli A., Wallis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
Eisenberg R.J., Wiley D.C.;
RT "Herpes simplex virus glycoprotein D bound to the human receptor
RL HveA.";
RN [7]
RP Mol. Cell 8:169-179(2001).
CC -1- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
CC TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
CC an important role in HSV pathogenesis because it enhanced the
CC entry of several wildtype HSV strains of both serotypes into CHO
CC cells, and mediated HSV entry into activated human T cells.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN LUNG, SPLEEN, AND THYMUS.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; U70321; AAB58354.1; -
CC EMBL; U81232; AAD00505.1; -
CC EMBL; AF153978; AAF75588.1; -
CC EMBL; AF373877; AAL47717.1; -
CC EMBL; AF373878; AAL47718.1; -
CC EMBL; BC002734; AAH02794.1; -
CC PDB; 1JMA; 25-SEP-01.
CC Genew; HGNC:11912; TNFRSF14.
```


NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
TISSUE=Lymphoid;
MEDLINE-97088617; PubMed-8934525;
Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
Graham C.J., Brown R., Farrow S.N.;
"A death-domain-containing receptor that mediates apoptosis.";
Nature 384:372-375(1996).
[2]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Umbilical vein endothelial cells;
MEDLINE-97081063; PubMed-8875942;
Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
"Signal transduction by DR3, a death domain-containing receptor
related to TNFR-1 and CD95.";
Science 274:990-992(1996).
[3]
SEQUENCE FROM N.A.
Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Heart;
MEDLINE-97148200; PubMed-8994832;
Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
Goddard A.D., Bauer K.D., Ashkenazi A.;
"Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-kappa-B.";
Curr. Biol. 6:1669-1676(1996).
[5]
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
MEDLINE-9722273; PubMed-9114039;
Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
McMichael A.J., Bell J.I.;
"LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
[6]
SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
MEDLINE-98113360; PubMed-9446802;
Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
Salles G.;
"A new death receptor 3 isoform: expression in human lymphoid cell
lines and non-Hodgkin's lymphomas.";
Biochem. Biophys. Res. Commun. 242:376-379(1998).
[7]
SEQUENCE FROM N.A. (ISOFORM 1).
Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE OF 4-417 FROM N.A.
TISSUE=Brain, and Fetal lung;
MEDLINE-97205335; PubMed-9052839;
Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
Browning J.L., MacDonald H.R., Tschopp J.;
"TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
Immunity 6:79-88(1997).
[9]
SEQUENCE OF 7-417 FROM N.A.
TISSUE=Brain;
Chaudhary P.M., Hood L.E.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Receptor for TNFSF12/AP03L/TWEAK. Interacts directly
with the adaptor TRADD. Mediates activation of NF-kappaB and
induces apoptosis. May play a role in regulating lymphocyte
homeostasis.
-1- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO

CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
CC and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
CC (potential).
CC -|- ALTERNATIVE PRODUCTS: 12 ISOFORMS; 1/WSL-1/LARD-1A (SHOWN HERE),
CC 2/LARD-1B, 3/WSL-S1/LARD-3, 4/WSL-S2/LARD-2, 5/LARD-4/LARD-11,
CC 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND
CC 12/BETA SOLUBLE; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -|- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC -|- PTM: GLYCOSYLATED (PROBABLE).
CC -|- SIMILARITY: CONTAINS 1 TNFR-CYS DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -|- CAUTION: Ref 5 reports for isoform 4 at position 208 a serine
CC residue instead of arginine.
CC -----
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CC -----
CC EMBL: Y09392; CAA70561.1; -
CC EMBL: Y09392; CAA70559.1; -
CC EMBL: Y09392; CAA70560.1; -
CC EMBL: U72763; AAC50819.1; -
CC EMBL: U83599; AAB41434.1; -
CC EMBL: U83600; AAB41435.1; -
CC EMBL: U78029; AAB40918.1; -
CC EMBL: U74611; AAB39714.1; -
CC EMBL: U94501; AAC51306.1; -
CC EMBL: U94504; AAC51309.1; -
CC EMBL: U94502; AAC51307.1; -
CC EMBL: U94503; AAC51308.1; -
CC EMBL: U94505; AAC51310.1; -
CC EMBL: U94506; AAC51311.1; -
CC EMBL: U94507; AAC51312.1; -
CC EMBL: U94508; AAC51313.1; -
CC EMBL: U94509; AAC51314.1; -
CC EMBL: U94510; AAC51315.1; -
CC EMBL: U94512; AAC51316.1; -
CC EMBL: U83598; AAB41433.1; -
CC EMBL: AF026070; AAC39556.1; -
CC EMBL: AF026071; AAB82288.1; -
CC EMBL: AB051850; BAB40662.1; -
CC EMBL: AB051851; BAB40663.1; -
CC EMBL: U75381; AAC51193.1; -
CC EMBL: U83597; AAB41432.1; -
CC Genew; HGNC:11910; TNFRSF12.
CC MIM; 603366; -
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC Pfam; PF00531; death; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00050; TNFR_NGFR_2; 1.
CC PROSITE; PS00017; DEATH_DOMAIN; 1.
CC Receptor; Apoptosis; Transmembrane; Alternative splicing; Signal;
KW Repeat; Polymorphism.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 417 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 25 199 SUPRACELLULAR MEMBER 12.
FT TRANSMEM 200 220 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 223 417 POTENTIAL.
FT REPEAT 34 71 CYTOPLASMIC (POTENTIAL).
FT REPEAT 72 115 TNFR-CYS 1.
FT REPEAT 116 163 TNFR-CYS 2.
FT REPEAT 116 163 TNFR-CYS 3.

FT REPEAT 164 192 TNFR-CYS 4.
FT DOMAIN 332 413 DEATH.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 48 61 BY SIMILARITY.
FT DISULFID 51 70 BY SIMILARITY.
FT DISULFID 73 89 BY SIMILARITY.
FT DISULFID 92 107 BY SIMILARITY.
FT DISULFID 95 115 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 138 155 BY SIMILARITY.
FT DISULFID 141 162 BY SIMILARITY.
FT DISULFID 165 176 BY SIMILARITY.
FT DISULFID 179 191 BY SIMILARITY.
FT DISULFID 187 195 BY SIMILARITY.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 54 98 MISSING (IN ISOFORM 6, ISOFORM 7 AND
FT VARSPLIC 54 236 MISSING (IN ISOFORM 8).
FT VARSPLIC 156 171 SRRTDCTGLFGEYE -> HPSVTILGQRPHPSSTS (IN
FT VARSPLIC 172 417 ISOFORM 7).
FT VARSPLIC 182 417 MISSING (IN ISOFORM 5 AND ISOFORM 6).
FT VARSPLIC 182 200 STLGSCPERCAAVCGWRQM -> PPSLAGAPMGAVQSAPV
FT VARSPLIC 182 218 LSVAGRGV (IN ISOFORM 11).
FT VARSPLIC 182 218 STLGSCPERCAAVCGWRQFWQVLLAGLVVPLLLGA ->
FT VARSPLIC 182 218 VLGPAGPWGPPGPPAWGHPDLHIPPLASQAPGYCR (IN
FT VARSPLIC 219 417 ISOFORM 3).
FT VARSPLIC 182 277 STLGSCPERCAAVCGWRQFWQVLLAGLVVPLLLGATLTY
FT VARSPLIC 182 277 TYRHCWPHKPLVTADAGMEALTPPPATHLSPLDSAHTLLA
FT VARSPLIC 182 277 PDSSEKICTVQLV -> PPSLAGAPMGAVQSAPVLSVAG
FT VARSPLIC 182 277 GRVGGVLMGRVGLWTEGRRVRGATTOHPPAFVSLGPG
FT VARSPLIC 182 277 APCWCPGPPAMGHPDLHIPPLASQAPGYCR (IN
FT VARSPLIC 278 417 ISOFORM 12).
FT VARSPLIC 200 253 MISSING (IN ISOFORM 12).
FT VARSPLIC 200 253 MFWQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADAG
FT VARSPLIC 200 253 MEALTPPPATHLS -> SRWCAGNARGRTGMDRGEAGEGG
Query Match 11.1%; Score 199.5; DB 1; Length 417;
Best Local Similarity 21.4%; Pred. No. 6.7e-08;
Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;
QY 56 GQFCHRPKPPGERKARDCTVNGDEPCVQCQEGKEYTDKAHFSKRCRCLCDGEGHLEV 115
Db 44 GLFCCRCGPAHYLKAPCTEPCGNSCLVCPQDTFLAWENHNHNSCARCQACQACQSOVA 103
QY 116 EINCTRTQNTKCRCKPNFF-----CNSTVCEHCDCTKC----- 149
Db 104 LENCASAVADTRCGCKPGWFVEQVSCVSSPFYCPCLDCGALHRRHRLLCSSRRDTCG 163
QY 150 -----EHGI-IKECTLTNTKKEE-----GSRSLNGLWCLLL--LPIPLIVVWRKE 194
Db 164 TCLPGFYERGDGCVSCTPTSLGSCPERCAAVCGWR-QMFWQVLLAGLVVPLLLGATLTY 222
QY 195 VQKTRKRR-----KENQ-----SHESPTLNPTVAINLSVDLSYITTI----- 236
Db 223 TYRHCWPHKPLVTADAGMEALTPPPATHLSPLDSAHTL---LAPPSSEKICTVQLVGN 279
QY 237 -----AGVMTLS----- 243
Db 280 SWTPGYPETOEALCPQVTSWDQLPSRALGPAAPATLSPSPSPAGSPAMMLQPGPOLYDVM 339
QY 244 -----QVKFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHQ 283
Db 340 DAVPARRWKEFVRTGLUREAIEAVEVE-IGRFDDQOQYEMLKWRQ 384
RESULT 9
ID T10A_HUMAN STANDARD; PRT; 468 AA.
AC 000220; Q96E62;
DT 16-OCT-2001 (Rel. 40, Created)

15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 10A precursor (Death receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL receptor-1) (TRAIL-R1).
TNFRSF10A OR DR4 OR TRAILR1 OR APO2.
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=97238921; PubMed=9082980;
Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Ebner R., Ni J., Dixit V.M.;
"The receptor for the cytotoxic ligand TRAIL.";
Science 276:111-113(1997).
[2]
SEQUENCE FROM N.A.
TISSUE=Ovary;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[3]
FUNCTION.
MEDLINE=98090092; PubMed=9430227;
Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
"Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway.";
Immunity 7:821-830(1997).
[4]
FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-kappaB.
[5]
SUBUNIT: Can interact with TRADD and RIP.
[6]
SUBCELLULAR LOCATION: Type I membrane protein.
[7]
TISSUE SPECIFICITY: Widely expressed. High levels are found in spleen, peripheral blood leukocytes, small intestine and thymus, but also in K562 erythroleukemia cells, MCF7 breast carcinoma cells and activated T-cells.
[8]
SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
[9]
SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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EMBL; U90875; AAC51226.1; --
EMBL; BC012866; AAHL2866.1; --
HSPG; 014763; IDOG.
Genew; HGNC:11904; TNFRSF10A.
MIM; 603611; --
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
Pfam; PF00531; death; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50030; TNFR_NGFR_2; 2.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL 1 23 POTENTIAL.
CHAIN 24 468 TUMOR NECROSIS FACTOR RECEPTOR
DOMAIN 24 239 SUPERFAMILY MEMBER 10A.
FT TRANSMEM 240 262 EXTRACELLULAR (POTENTIAL).
FT

RT "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";
RL EMBO J. 16:5386-5397(1997).
RN [2]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE
RX SPLICING.
RA Sreaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,
RA McMichael A.J., Bell J.I.;
RT "TRICK2, a new alternatively spliced receptor that transduces the
RT cytotoxic signal from TRAIL.";
RL Curr. Biol. 7:693-696(1997).
RN [3]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.
RX TISSUE=Liver, and Spleen;
RA MEDLINE=98039016; PubMed=9373179;
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,
RA Tschoep J.;
RT "Characterization of two receptors for TRAIL.";
RL FEBS Lett. 416:329-334(1997).
RN [4]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX TISSUE=Ovary;
RA MEDLINE=97467719; PubMed=9326928;
RA Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,
RA Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,
RA Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;
RT "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor
RT gene.";
RL Nat. Genet. 17:141-143(1997).
RN [5]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=97390508; PubMed=9242610;
RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL.";
RL Science 277:815-818(1997).
RN [6]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=97467318; PubMed=9325248;
RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.;
RT "Identification and molecular cloning of two novel receptors for the
RT cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 272:25417-25420(1997).
RN [7]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=98090092; PubMed=9430227;
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";
RL Immunity 7:821-830(1997).
RN [8]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=97390509; PubMed=9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.;
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors.";
RL Science 277:818-821(1997).
RN [9]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2
RT gene in colorectal carcinoma.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RA Cao X., Zhang W., Wan T.;
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RA Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;

RT "Homo sapiens homolog of tumor necrosis factor receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
RX MEDLINE=20017054; PubMed=10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.
RX PubMed=10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Sreaton G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).
CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
CC adaptor molecule FADD recruits caspase-8 to the activated
CC receptor. The resulting death-inducing signaling complex (DISC)
CC performs caspase-8 proteolytic activation which initiates the
CC subsequent cascade of caspases (aspartate-specific cysteine
CC proteases) mediating apoptosis. Promotes the activation of NF-
CC kappaB.
CC -!- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/TRICK2B (SHOWN HERE)
CC AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING
CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;
CC very highly expressed in tumor cell lines such as HeLa S3, K562,
CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral
CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,
CC ovary, uterus, placenta, testis, esophagus, stomach and throughout
CC the intestinal tract; not detectable in brain.
CC -!- INDUCTION: TNFSF10B is regulated by the tumor suppressor p53.
CC -!- DISEASE: Defects in TNFSF10B may be a cause of squamous cell
CC carcinoma of the head and neck.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF016849; AAC51778.1; -
DR EMBL; AF018657; AAB70577.1; -
DR EMBL; AF018658; AAB70578.1; -
DR EMBL; AF016266; AAB81180.1; -
DR EMBL; AF022386; AAB71949.1; -
DR EMBL; AF012628; AAB67109.1; -
DR EMBL; AF020501; AAB71412.1; -
DR EMBL; AF016268; AAC01565.1; -
DR EMBL; AF012535; AAB67103.1; -
DR EMBL; AB014718; BAA33723.1; -
DR EMBL; AB014710; BAA33723.1; JOINED.
DR EMBL; AB014711; BAA33723.1; JOINED.
DR EMBL; AB014712; BAA33723.1; JOINED.
DR EMBL; AB014713; BAA33723.1; JOINED.
DR EMBL; AB014714; BAA33723.1; JOINED.
DR EMBL; AB014715; BAA33723.1; JOINED.
DR EMBL; AB014716; BAA33723.1; JOINED.
DR EMBL; AB014717; BAA33723.1; JOINED.
DR EMBL; AF153687; AAF75587.1; -

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DR EMBL; AF192548; AAF07175.1; -
DR EMBL; BC001281; AAH01281.1; -
DR Genew; HGNC:11905; TNFRSF10B.
DR MIM; 603612; -
DR PDB; 1D0G; 22-OCT-99.
DR PDB; 1D4V; 01-NOV-99.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Transmembrane; Repeat; Signal;
KW Alternative splicing; 3D-structure.
FT SIGNAL 1 55
FT CHAIN 56 440
      TUMOR NECROSIS FACTOR RECEPTOR
      SUPERFAMILY MEMBER 10B.
      EXTRACELLULAR (POTENTIAL).
      POTENTIAL.
      CYTOPLASMIC (POTENTIAL).
      TNFR-CYS 1.
      TNFR-CYS 2.
      TNFR-CYS 3.
      TAPE.
      DEATH.
      POLY-GLY.
      DOMAIN 56 210
      TRANSMEM 211 231
      DOMAIN 232 440
      REPEAT 57 94
      REPEAT 97 137
      REPEAT 138 178
      REPEAT 192 206
      DOMAIN 339 422
      DOMAIN 422 440
      DISULFID 81 94
      DISULFID 97 113
      DISULFID 116 129
      DISULFID 119 137

Query Match
Best Local Similarity 26.6%; Score 197; DB 1; Length 440;
Matches 77; Conservative 34; Mismatches 93; Indels 86; Gaps 14;

QY 8 LPLVLTGVARLSKSNVAQYTDINSKGL--ELRKTVTVTQNLGLHDPGQCHRPCKPP 65
DB 38 LVLVAVALL-----VSAESALITQDLAPQRAAPQKRSPSEGL-----CPP 83
QY 66 GERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDGHLGVEIN-CTRQTN 124
DB 84 GH-----ISEGRCISCKYQDYSTHWNDLLFLCRLCTRCDSG---EVELSPCTTRN 134
QY 125 TKCRKPNCFTVCEHCDPC-TKEHGIK--ECTLTSTNRC--KEGSRNLSGLWCL 179
DB 135 TVCQCEGTFRFEDSPDMCRKRTGCPGMVKVGDCTPWSIDICVHESGT-----185
QY 180 LLLPIPLIVWKRKEVQKCRKRKENQSHESPTINPTVAINLSVDLSKYI---TTIA 237
DB 186 -----KHSGAPAVEETVTSPTGTPA---SPCSLSGLIIGVTVA 221
QY 238 GVM-----TLQVKGVKRVKNGVNEAKIDEIK-----NDNV 267
DB 222 AVLLIVAVFVCKSLWKVLPYLKIGCSGGGDPERVDRSORPGAEDNV 271

RESULT 11
TR23_MOUSE
ID TR23_MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q8VHCO;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN TNFRSF23 OR TNFRSF11 OR TNFRH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pan G., Mao W., Risser P.;
RT "Characterization of SOB, a member of the TNFR family.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -----
```

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EMBL; AJ278264; CAC16405.1; -
EMBL; AJ276505; CAC27352.1; -
EMBL; AY046550; AAL05072.1; -
HSSP; P19438; 1EXT.
MGD; MGI:1930269; Tnfrsf23.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 31 176 EXTRACELLULAR (POTENTIAL).
FT REPEAT 37 72 TNFR-CYS 1.
FT REPEAT 74 114 TNFR-CYS 2.
FT REPEAT 115 155 TNFR-CYS 3.
FT DISULFID 38 49 BY SIMILARITY.
FT DISULFID 50 63 BY SIMILARITY.
FT DISULFID 53 72 BY SIMILARITY.
FT DISULFID 75 90 BY SIMILARITY.
FT DISULFID 93 106 BY SIMILARITY.
FT DISULFID 96 114 BY SIMILARITY.
FT DISULFID 116 131 BY SIMILARITY.
FT DISULFID 134 147 BY SIMILARITY.
FT DISULFID 137 155 BY SIMILARITY.
FT CARBOHYD 148 148 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DDB7D CRC64;
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Query Match
Best Local Similarity 10.5%; Score 189.5; DB 1; Length 176;
Matches 42; Conservative 19; Mismatches 68; Indels 7; Gaps 5;
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QY 50 EGLHHDGFCFKPCPPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDE 109
DB 40 DGEYQSDNVCCCKTSPGTFVKAAPKPIPTQGGCKCHPG-TFTGKNGLHDCELSTCDK 98
QY 110 GHGLEVEINCFRTQNTKCRKRN-PFCNSTVCEHCDPCTKEHGI--INCKTLTNTKCK 166
DB 99 DONMYAD--CSATDRKCEQIGLYYDPKFPESCRPCTKCPQGPVPLQECNSTANTVCS 156
QY 167 EEGSRNLGWLCLLL 182
DB 157 SSVSNPR-NWLFLLML 171
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RESULT 12
T11B_RAT
ID T11B_RAT STANDARD; PRT; 401 AA.
AC O08727;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 11b precursor
DE (Osteoprotegerin).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Upregulated by osteopontin.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC -----
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CC -----
DR EMBL; U94330; AAB53707.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 64 80

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FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
SQ SEQUENCE 401 AA; 46192 MW; FECSA31FD4E573A CRC64;
Query Match 10.3%; Score 186; DB 1; Length 401;
Best Local Similarity 25.8%; Pred. No. 6.6e-07;
Matches 77; Conservative 36; Mismatches 110; Indels 76; Gaps 16;
QY 42 TTVETQNLEGLHHDGQ-----FCHKPCPPGKERKARDCTVNGDEPCVPCQSGKEVTKAH 96
DB 19 TTOETFPKYLHYDPETGROLLCDK-CAPGYLKHQCTVR-RKTLGVPCPD-YSTDSWH 75
QY 97 FSSKRCRCR-LCDGSHGLEVEINCTRONTKCRCKPNFFCNSTVC---EHGDP----- 145
DB 76 TSDECVYCSVCKELQVKB--CNRTHNRVCEEGRYLEFCLKHKRSPGGLGVLOA 133
QY 146 -----CTKCEHGIIKECTLTSTKCEGSRNSLGLCLLLPIPIIYVVRKEVQR 197
DB 134 GTPERNTVCKRCPDGFSGET-SSKAPCRKHTNCSSLG---LLL-----IQK 176
QY 198 -----TCRKHREKNOGSHESPINPE-----TVAINLSDVDLSKYITTTAGVWTL 245
DB 177 GNATHDNVCSGNREATQCGIDVTLCSEAFPAVPTKIIIPNWLVSVDLSLPGTK----- 231
QY 246 KGFVRKNGVNEAKIDEIKNDNVQDTAQKVOLLRNHQLHGCKEAYDTFLIKDLKKANLC 304
DB 232 -----VNAESVERIKRRH--SSQETFOLLKLKHKHQDNQEMVKIIQDI---DLC 277
RESULT 13
TNR3_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE protein) (Tumor necrosis factor C receptor).
GN LYBR OR TNFRSF3 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hcdNA library of human 12p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RA MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
RN [4]

```

Query Match	10.3%	Score 185.5	DB 1	Length 435
Best Local Similarity	25.3%	Pred. No. 7.9e-07		
Matches	63	Conservative 25	Mismatches 82	Indels 79
				Gaps 12
QY	43	TVETQNLGLHHDGQFCHKPCPPGERKARDCTVNGDEPCVPCQGEKGYDKAHFSKCR	102	
db	42	TCRDOEKEYEPQHRITCCSRCPGTVVSAKCSRIRTV-CATCAE-NSYNEHWNYLTICQ	99	

Characterization of monomeric and homodimeric forms of osteoclastogenesis inhibitory factor.;
Biochem. Biophys. Res. Commun. 245:382-387(1998).
[6]
SEQUENCE OF 22-393 FROM N.A.
TISSUE-Placenta;
He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
Cloning and expression of osteoprotegerin from Homo sapiens.;
Acta Biochim. Biophys. Sin. 31:680-684(1999).
[7]
SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
MEDLINE-97312536; PubMed-9168977;
Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
Morinaga T., Higashio K.;
Isolation of a novel cytokine from human fibroblasts that specifically inhibits osteoclastogenesis.;
Biochem. Biophys. Res. Commun. 234:137-142(1997).
[8]
TRAIL BINDING.
MEDLINE-98269100; PubMed-9603945;
Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
James I.E., Rosenberg M., Lee J.C., Young P.R.;
Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.;
J. Biol. Chem. 273:14363-14367(1998).
[9]
CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
MEDLINE-98148058; PubMed-9478964;
Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
Morinaga T., Higashio K.;
Characterization of structural domains of human osteoclastogenesis inhibitory factor.;
J. Biol. Chem. 273:5117-5123(1998).
[10]
REVIEW
MEDLINE-21395914; PubMed-11505389;
Hofbauer L.C., Neuber A., Heufelder A.E.;
Receptor activator of nuclear factor-kappaB ligand and osteoprotegerin: potential implications for the pathogenesis and treatment of malignant bone diseases.;
Cancer 92:460-470(2001).
CC
-1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.
CC
-1- SUBUNIT: Homodimer.
CC
-1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney, liver, spleen, thymus, prostate, ovary, small intestine, thyroid, lymph node, trachea, adrenal gland, testis, and bone marrow. Detected at very low levels in brain, placenta and skeletal muscle. Highly expressed in fetal kidney, liver and lung.
CC
-1- INDUCTION: Upregulated by increasing calcium concentration in the medium and estrogens. Downregulated by glucocorticoids.
CC
-1- PTM: N-glycosylated. Contains sialic acid residues.
CC
-1- PTM: N-terminus may be blocked.
CC
-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
-1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC

CC
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CC

CC
EMBL; U94332; AAB53709.1; -;
DR
EMBL; AB002146; BAA25910.1; -;
DR
EMBL; AB008822; BAA32076.1; -;

DR EMBL; AB008821; BAA32076.1; JOINED.
DR EMBL; BC030155; AAB30155.1; -;
DR EMBL; AF134187; AAF20168.1; -;
DR HSP; P25942; ICDF.
DR Genew; HGNC:11909; TNFRSF11B.
DR MIM; 602643; -;
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS0652; TNFR_NGFR_1; 2.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1
FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 11B.
FT REPEAT 24 62 TNFR-CYS 1.
FT REPEAT 65 105 TNFR-CYS 2.
FT REPEAT 107 142 TNFR-CYS 3.
FT REPEAT 145 185 TNFR-CYS 4.
FT DOMAIN 198 269 DEATH 1.
FT DOMAIN 270 365 DEATH 2.
FT SITE 400 400 INVOLVED IN DIMERIZATION.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT DISULFID 166 185 BY SIMILARITY.
FT CARBOHYD 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 3 K -> N.
FT /FTid-VAR_013439.
FT MUTAGEN 400 400 C->S: ABOLISHES DIMERIZATION.
FT MUTAGEN 400 401 MISSING: ABOLISHES DIMERIZATION.
FT CONFLICT 263 263 D -> A (IN REF. 1).
SQ SEQUENCE 401 AA; 46040 MW; EDF448B67D86C71E CRC64;
Query Match 10.18; Score 183; DB 1; Length 401;
Best Local Similarity 25.98; Pred. No. 1.1e-06;
Matches 75; Conservative 35; Mismatches 122; Indels 58; Gaps 13;
QY 42 TTVTQNEGLHHDGQFCHK-PCPPGERKARDCTVNGDEPCVQCEGKEYTDKAHF 97
DB 19 TTQETFPKYLHYDEETSHQLLCKDCKPGTYLKQCTAKW-KTVCAPCPD-HYYTDSWHT 76
QY 98 SSKRRRCR-LCDEGHGGLVEINCTRTQNTKCRKPFNCSTVC---EHCDDPTCKEHI 153
DB 77 SDELYCSPVCKELQYVKQE--CNRTNRCVCEKGRYLETEFCLKHRSPPD---GFGV 130
QY 154 IKECTLTISNTCKE--EGSRNGLWGLCLLLPIPLVWVRKEVQKTCRKH----- 202
DB 131 VQAGTPTERTVCKRCPDGFSSN-----ETSSKAPCRKHTKNCVFGLL 172
QY 203 --RENOQSHESPTLNPTVAINLSVDLSKYITTIAGVMT-----LSOVKGFYKNGV 254
DB 173 LTQGNATHDNCISNSESCKGIDVTLCCEAFRAFPVTKFTPNWLSVLVDNLPQTKV 232
QY 255 NEAKIDEIKNDVQDTAQKYLQRLNHWLHGLHGKKEAYDTLTKDLKKNALC 304
DB 233 NAESVERIKRQH--SSQQTQLLKLWKLHQNKKQDQIVKKIIDI---DLC 277
RESULT 15

T11B_MOUSE
 ID T11B_MOUSE STANDARD; PRT; 401 AA.
 AC 008712; 070202;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 GN TNFRSF11B OR OPB OR OCIF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Kidney;
 RA MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 RA of bone density.";
 RT Cell 89:309-319(1997).
 RL [2]
 RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
 RP AND ARG-296.
 RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
 RA MEDLINE=98382527; PubMed=9714833;
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
 RA Higashio K.;
 RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
 RA gene and its expression in embryogenesis.";
 RT Gene 215:339-343(1998).
 RL [3]
 RP FUNCTION.
 RA MEDLINE=21060987; PubMed=10952716;
 RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
 RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
 RA Simonet W.S.;
 RA "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
 RA osteoclasts and prevents vascular calcification by blocking a process
 RA resembling osteoclastogenesis.";
 RT J. Exp. Med. 192:463-474(2000).
 RL [4]
 RP FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 RP its function in osteoclastogenesis. Inhibits the activation of
 RP osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 RP homeostasis seems to depend on the local RANKL/OPG ratio. May also
 RP play a role in preventing arterial calcification. May act as decoy
 RP receptor for TRAIL and protect against apoptosis. TRAIL binding
 RP blocks the inhibition of osteoclastogenesis.
 CC [5]
 RP SUBUNIT: Homodimer.
 CC [6]
 RP SUBCELLULAR LOCATION: Secreted.
 CC [7]
 RP TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
 CC intestines and calvaria. Highly expressed in decidua and placenta,
 CC and in embryo.
 CC [8]
 RP DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
 CC whereas expression decreases at day 11 and increases from day 15
 CC to 17. On day 15 found in developing bone primordia,
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,
 CC abdominal aorta and midgut.
 CC [9]
 RP INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
 CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
 CC [10]
 RP SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC [11]
 RP SIMILARITY: CONTAINS 2 DEATH DOMAINS.
 CC [12]
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 DR EMBL; U94331; AAB53708.1; -;
 DR EMBL; AB013898; BAA28269.1; -;
 DR EMBL; AB013903; BAA33388.1; -;
 DR EMBL; AB013899; BAA33388.1; JOINED.
 DR EMBL; AB013900; BAA33388.1; JOINED.
 DR EMBL; AB013901; BAA33388.1; JOINED.
 DR EMBL; AB013902; BAA33388.1; JOINED.
 DR HSSP; P25942; ICDP.
 DR MGI; MGI:109587; Tnf1b1b.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR ProDom; PD000771; TNFR_C6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00017; DEATH DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT FT BY SIMILARITY.
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 11B.
 FT REPEAT 24 62
 FT REPEAT 65 105
 FT REPEAT 107 142
 FT REPEAT 145 185
 FT DOMAIN 198 269
 FT DOMAIN 283 365
 FT SITE 400 400
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 107 115
 FT DISULFID 124 142
 FT DISULFID 145 160
 FT DISULFID 166 185
 FT CARBOHYD 98 98
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 138 138
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA; 45923 MW; CA6102D3B312470 CRC64;
 SQ
 Query Match 10.1%; Score 182; DB 1; Length 401;
 Best Local Similarity 25.5%; Pred. No. 1.3e-06;
 Matches 76; Conservative 34; Mismatches 114; Indels 74; Gaps 15;
 QY 42 TTVEQNLEGLHHDGQFCHK----PCPCERKARCTVNGDEPDCVPCQEGKEYTDKAHF 97
 DB 19 TQETPLPKYLYHDETGHQLLCKDCAPCTYLKQCTVR-RKTLCPVCPD-HSYTDSWHT 76
 QY 98 SSKRCRR-LCDEGHGHEVEINCTQTQTKRCNFFCNSTVC---EHCDD-----145
 DB 77 SDECVICSPVKELQSVQKE--CNETHRVCECEGRYLETEFCLKHKRSCPPGSGVQAG 134
 QY 146 -----CTKEHGIIKCTTSTNTKCEGSRSLGWLCLLLPLIYVVRKEVQK- 197
 DB 135 TPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFG-----LLL-----IQKG 177

[illegible]

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Job time : 18.6873 secs

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